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OM protein - protein search, using sw model

Run on: August 28, 2004, 01:30:52 ; Search time 124 Seconds

(without alignments)
448.886 Million cell updates/sec

Title: US-10-003-211-1

Perfect score: 1133

Sequence: 1 SQPQAVPPVASENQTCDQE.....QSDTCKNPDEPPENSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_geneseq_29JAn04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------------|
| 1 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 2 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 3 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 4 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 5 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 6 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 7 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 8 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 9 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 10 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 11 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 12 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 13 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 14 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 15 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 16 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 17 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 18 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 19 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 20 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 21 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 22 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 23 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 24 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |
| 25 | 1133 | 100.0 | 197 | 2 | AAW23220 Extracellular |

| | | | | | |
|----|-----|------|-----|---|--------------------|
| 26 | 305 | 26.9 | 235 | 4 | AAB37685 Human 40 |
| 27 | 305 | 26.9 | 235 | 6 | ADA20593 Human 40x |
| 28 | 305 | 26.9 | 248 | 3 | AAV94718 Human typ |
| 29 | 305 | 26.9 | 355 | 6 | ADA09891 Human rec |
| 30 | 305 | 26.9 | 461 | 2 | AAI11141 Human TNF |
| 31 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 32 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 33 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 34 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 35 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 36 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 37 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 38 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 39 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 40 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 41 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 42 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 43 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 44 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |
| 45 | 305 | 26.9 | 461 | 2 | AAI11001 40KD TNF |

ALIGNMENTS

RESULT 1
AAW23220 standard; protein; 197 AA.

29-0CT-1997 (first entry)

Extracellular domain of human lymphotoxin beta receptor.

Human; lymphotoxin beta; receptor; blocking agent; extracellular;
ligand binding; domain; treatment; Th1 cell; immune response; delayed;
hypersensitivity; contact; tuberculosis; granulomatous; graft versus host;
disease; organ rejection; autoimmune; disorder; multiple sclerosis;
insulin dependent diabetes; uveitis; cytokine; sympathetic ophthalmia;
psoriasis; disteria; Toxoplasma; infection; Mycobacterium; abnormal;
lymphoid organ; development.

Homo sapiens.

W09703687-A1.

06-FEB-1997.

19-JUL-1996; 96WO-US012010.

21-JUL-1995; 95US-00505606.

(BIOJ) BIOGEN INC.

Browning JL, Benjamin CD, Hochman PS;

WPI; 1997-132373/12.

Compositions comprising lymphotoxin-beta receptor blocking agent - used
to treat autoimmune diseases, e.g. sclerosis, insulin-dependent
diabetes, etc.

Example 1; Page 55-56; 76pp; English.

The present sequence, a human lymphotoxin beta receptor (LT-beta-R)
blocking agent, comprises the extracellular ligand binding domain of the
human LT-beta-R up to the transmembrane region. It can be used to treat a
Th1 cell mediated immune response which contributes to a delayed type
hypersensitivity reaction, preferably contact, tuberculin type or
granulomatous hypersensitivity, graft versus host disease, organ
rejection or an autoimmune disorder, i.e. multiple sclerosis, insulin
dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can

CC also be used to treat conditions exacerbated by the activities of Th-1
CC type cytokines, or *Listeria*, *Toxoplasma* or *Mycobacterium* infection. Its
CC ability to selectively or partially block the LT-beta-R pathway may be
CC useful in the treatment of abnormal lymphoid organ development associated
CC with misexpression or overexpression of signalling by the LT-beta-R
CC pathway. The present LT-beta-R blocking agent is capable of selectively
CC inhibiting Th1, but not Th2 cell dependent immune effector mechanisms. As
CC Th1 cytokines can inhibit Th2 cell dependent responses, the present LT-
CC beta-R blocking agent may also indirectly stimulate certain Th2 cell
CC dependent responses which are normally inhibited by Th1 induced
CC cytokines. Doses of about 1 mg/kg of the present soluble LT-beta-R are
CC expected to be suitable starting doses for optimising treatment
CC
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGGTVYSAKCSIRIDTVCAATCAENS 60
DB 1 SQPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGGTVYSAKCSIRIDTVCAATCAENS 60
QY 61 YNEHMYLTITCOLCRPCDPVWGLEBETAPCTSKRTQCRCPGMFCAMALECTHCELLSD 120
DB 61 YNEHMYLTITCOLCRPCDPVWGLEBETAPCTSKRTQCRCPGMFCAMALECTHCELLSD 120
QY 121 CPFGTEBELKDEYVGKGNHCVPCKAGHFONTSSPSARCOPTHRCENGLVEAAGTAQSD 180
DB 121 CPFGTEBELKDEYVGKGNHCVPCKAGHFONTSSPSARCOPTHRCENGLVEAAGTAQSD 180
QY 181 TTCNPLEPLPPEMSGT 197
DB 181 TTCNPLEPLPPEMSGT 197

RESULT 2
AAV31326
ID AAV31326 standard; peptide; 197 AA.

XX AAY31326;

AC AAY31326;

XX 04-OCT-1999 (first entry)

DE Human lymphotoxin (LT) beta-receptor extracellular region.

XX Lymphotoxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell;
KW immune system; tumour; follicular lymphoma; extracellular domain; human.

XX Homo sapiens.

OS Homo sapiens.

PN WO938525-A1.

XX WO938525-A1.

PD 05-AUG-1999.

XX 05-AUG-1999.

PF 29-JAN-1999; 99WO-US001928.

XX 29-JAN-1999; 99WO-US001928.

PR 30-JAN-1998; 98US-0073112P.

XX 30-JAN-1998; 98US-0073112P.

PA 02-FEB-1998; 98US-0073410P.

XX 02-FEB-1998; 98US-0073410P.

XX (BIOJ) BIOGEN INC.

XX (BIOJ) BIOGEN INC.

XX Browning J, Thorbecke J, Tsiangbe V;
XX PI MPI; 1999-469242/39.
XX DR MPI; 1999-469242/39.
XX PT New method of treating follicular lymphomas by inhibiting interaction
XX PT between lymphotoxin-beta and its receptor.
XX PS Example 1; Page 25-26; 31pp; English.
XX The invention provides a method for arresting or reducing severity of
XX effects of a tumour by administration of a composition which inhibits the

CC interaction between lymphotoxin (LT) beta and its receptor. An inhibitor
CC of the interaction between LT-beta and its receptor can be administered
CC for altering the survival or maintenance of follicular dendritic cells in
CC a subject and for altering the architecture of the organs of the immune
CC system. The method is useful for treating tumours, specifically
CC follicular lymphomas. It offers an alternative therapy for those with
CC tumours resistant to traditional chemotherapy. The present sequence
CC represents the extracellular region of the human LTbeta-receptor and
CC comprises the ligand binding domain
CC
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGGTVYSAKCSIRIDTVCAATCAENS 60
DB 1 SQPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGGTVYSAKCSIRIDTVCAATCAENS 60
QY 61 YNEHMYLTITCOLCRPCDPVWGLEBETAPCTSKRTQCRCPGMFCAMALECTHCELLSD 120
DB 61 YNEHMYLTITCOLCRPCDPVWGLEBETAPCTSKRTQCRCPGMFCAMALECTHCELLSD 120
QY 121 CPFGTEBELKDEYVGKGNHCVPCKAGHFONTSSPSARCOPTHRCENGLVEAAGTAQSD 180
DB 121 CPFGTEBELKDEYVGKGNHCVPCKAGHFONTSSPSARCOPTHRCENGLVEAAGTAQSD 180
QY 181 TTCNPLEPLPPEMSGT 197
DB 181 TTCNPLEPLPPEMSGT 197

RESULT 3
ABP6137
ID ABP6137 standard; protein; 435 AA.

XX ABP6137;

XX 09-MAY-2003 (first entry)

DE Human TNF receptor 2 related protein/LTRbeta SEQ ID NO:19.

XX Human; tumour necrosis factor receptor 2 related protein variant;
KW TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;
KW TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;
KW asthma; ulcerative colitis.

XX Homo sapiens.

OS Homo sapiens.

PN WO2003012037-A2.

XX WO2003012037-A2.

PD 13-FEB-2003.

XX 13-FEB-2003.

PF 24-JUL-2002; 2002WO-US023684.

XX 24-JUL-2002; 2002WO-US023684.

PR 27-JUL-2001; 2001US-00917372.

XX 27-JUL-2001; 2001US-00917372.

PA (INCY-) INCYTE GENOMICS INC.

XX (INCY-) INCYTE GENOMICS INC.

PI Lal PG, Warren BA;

XX Lal PG, Warren BA;

DR MPI; 2003-256445/25.

XX MPI; 2003-256445/25.

XX New cDNA, useful for preparing a composition for treating a disease or
XX PT condition associated with increased TNF signaling e.g., cancer of the
XX PT prostate, ovary, gallbladder, breast, brain, liver or colon, or
XX PT rheumatoid arthritis, asthma.
XX Disclosure; Fig 2A-C; 64pp; English.
XX The present invention describes human tumour necrosis factor receptor 2
XX related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic

CC and immunosuppressive activities, and can be used in gene therapy. The
CC TNFR2PV cDNA or protein sequences can be used for preparing a composition
CC for treating a disease or condition associated with increased TNF
CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,
CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
CC arthritis, asthma or ulcerative colitis. The present sequence represents
CC a human TNFR2 related protein/LTRbeta amino acid sequence, which is given
CC in comparison with human TNFR2PV in the exemplification of the present
CC invention
CC
CC
SQ Sequence 435 AA;
Query Match 100.0%; Score 1133; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQPQAVPPYASENQTCRDOEKEYEPQHRICCSRCPPGTYSACSRIRDTVCATCAENS 60
Db 28 SQPQAVPPYASENQTCRDOEKEYEPQHRICCSRCPPGTYSACSRIRDTVCATCAENS 87
QY 61 YNEHWNVLTITCOLCRPCDPVWGLEIAPCTSKRTQCRQCPGMCAAMALECTHCELLSD 120
Db 88 YNEHWNVLTITCOLCRPCDPVWGLEIAPCTSKRTQCRQCPGMCAAMALECTHCELLSD 147
QY 121 CPPTGEALKDVEGKGNHCVPCAKGHONTSSPSARQCPHTRCENOGIVAAAGTAQSD 180
Db 148 CPPTGEALKDVEGKGNHCVPCAKGHONTSSPSARQCPHTRCENOGIVAAAGTAQSD 207
QY 181 TTCNPLEPLPEMSGT 197
Db 208 TTCNPLEPLPEMSGT 224
RESULT 4
ID ABR40220 standard; protein: 435 AA.
XX ABR40220;
AC 12-JUN-2003 (first entry)
DT
XX
XX Human genoxin.
KM Human; genoxin; antiarteriosclerotic; anti-diabetic; hypotensive;
KM anti-inflammatory; anorectic; immunomodulator; cytostatic; anti-HIV;
KM anti-inflammatory; cardiant; cerebroprotective; gene therapy;
KM tumour necrosis factor receptor; TNFR; body mass; weight loss; obesity.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein /label= Signal_peptide 31..435
FT Domain /label= Mature_genoxin 31..227
FT Domain /label= Extracellular_domain 228..248
FT Domain /label= Transmembrane_domain 249..435
FT Domain /label= Intracellular_domain
XX
XX
XX WO2003011322-A1.
XX
XX 13-FEB-2003.
XX
XX 31-JUL-2002; 2002WO-IB003417.
XX
XX 02-AUG-2001; 2001US-0309917P.
XX
XX (GHEST) GENSET SA.
XX
XX Lucas J, Djalynas D, Briggs K;

XX WP1; 2003-256417/25.
DR N-PSDB; ABZ99578.
XX
XX Screening for an agonist or antagonist of Genoxin activity, useful for
PT preventing or treating metabolic disorders, comprises contacting Genoxin
PT polypeptide with a test compound and determining binding.
XX
XX
PS Example 10; Page 33-34; 37pp; English.
XX
XX The invention relates to a novel method for screening for an agonist or
CC antagonist of Genoxin activity. The agonists/antagonists of the invention
CC have antiarteriosclerotic, anti-diabetic, hypotensive, anti-inflammatory,
CC anorectic, immunomodulator, cytostatic, anti-HIV, anti-inflammatory,
CC cardiant, and cerebroprotective activity. The polypeptides of the
CC invention may have a use in gene therapy, and act as tumour necrosis
CC factor receptor (TNFR) agonists. The method is used to screen for an
CC agonist or antagonist of Genoxin. The method is useful in metabolic
CC research, particularly, in discovering compounds that modulate Genoxin
CC activity or that reduce or increase body mass and maintain weight loss,
CC and in preventing or treating obesity-related diseases or disorders such
CC as hyperlipidaemia, atherosclerosis, heart disease, stroke, insulin-
CC resistant diabetes or hypertension, or for preventing or treating
CC disorders associated with excessive weight loss, such as cachexia, cancer
CC -related weight loss, acquired immunodeficiency syndrome (AIDS)-related
CC weight loss, chronic inflammatory disease-related weight loss, or
CC anorexia. The present sequence represents the human genoxin of the
CC invention
XX
SQ Sequence 435 AA;
Query Match 100.0%; Score 1133; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQPQAVPPYASENQTCRDOEKEYEPQHRICCSRCPPGTYSACSRIRDTVCATCAENS 60
Db 28 SQPQAVPPYASENQTCRDOEKEYEPQHRICCSRCPPGTYSACSRIRDTVCATCAENS 87
QY 61 YNEHWNVLTITCOLCRPCDPVWGLEIAPCTSKRTQCRQCPGMCAAMALECTHCELLSD 120
Db 88 YNEHWNVLTITCOLCRPCDPVWGLEIAPCTSKRTQCRQCPGMCAAMALECTHCELLSD 147
QY 121 CPPTGEALKDVEGKGNHCVPCAKGHONTSSPSARQCPHTRCENOGIVAAAGTAQSD 180
Db 148 CPPTGEALKDVEGKGNHCVPCAKGHONTSSPSARQCPHTRCENOGIVAAAGTAQSD 207
QY 181 TTCNPLEPLPEMSGT 197
Db 208 TTCNPLEPLPEMSGT 224
RESULT 5
ID ABR09821 standard; protein: 435 AA.
XX ABR09821;
AC
XX
XX 10-JUL-2003 (first entry)
DT
XX
XX TNF-receptor associated factor 5 (TRAF5) interacting protein #1.
XX
XX Human; cytostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer;
KM TNF-receptor associated factor 5 interacting protein;
KM tumour necrosis factor associated factor 5 interacting protein;
KM TRAF5 interacting protein.
XX
XX Homo sapiens.
XX
XX WO2003031571-A2.
XX
XX 17-APR-2003.

PF 02-OCT-2002; 2002MO-US031357.
 XX
 PR 05-OCT-2001; 2001US-0327454P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 25-JUN-2002; 2002US-0391342P.
 PR 01-OCT-2002; 2002US-00262445.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Alsobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A;
 PI Edinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kekuda R;
 PI Mezes PS, Millet I, Ooi CE, Patturajan M, Rieger DK, Splet KA;
 PI Taupier RJ, Zernhuesen BD, Zhong H, Zhong M;
 XX WPI; 2003-381704/36.
 DR N-PSDB; ACA90237.
 XX
 PT New DAPK3 polypeptide, useful for preparing a composition for treating or
 PT preventing e.g., cancer.
 XX
 PS Example 20F; Page 240; 253pp; English.
 XX
 CC The invention describes an isolated polypeptide comprising any of 33 90-
 CC 1273 amino acid sequences (I) given in the specification or its mature
 CC form, a sequence that is at least 95 % identical to (I), or a sequence
 CC comprising one or more conservative substitutions in the amino acid
 CC sequence of (I). The polypeptide is useful for preparing a composition
 CC for treating or preventing e.g., cancer. This is the amino acid sequence
 CC of a tumour necrosis factor (TNF)-receptor associated factor 5 (TRAF5)
 CC interacting protein associated with the identification of novel human
 CC proteins and their functions
 CC
 XX
 SQ Sequence 435 AA;
 Query Match 100.0%; Score 1133; DB 6; Length 435;
 Best Local Similarity 100.0%; Pred. No. 2.3e-78;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPQAVPYASBNQTCRDOEKERYEPQHRICCSRCPGGTVYSAKCSRIRDTVCATCAENS 60
 DB 28 SOPQAVPYASBNQTCRDOEKERYEPQHRICCSRCPGGTVYSAKCSRIRDTVCATCAENS 87
 QY 61 YNEHNNYLTICQLCRPCDPVWGLIEIAPCTSRKTKQCRQCPGMFCAAMALECTHCELLSD 120
 DB 88 YNEHNNYLTICQLCRPCDPVWGLIEIAPCTSRKTKQCRQCPGMFCAAMALECTHCELLSD 147
 QY 121 CEPGTAEIKDEVGKGNHNCVPCAKGHPONTSSPSARCOPIHRCENOGIVEAAPGTQSD 180
 DB 148 CEPGTAEIKDEVGKGNHNCVPCAKGHPONTSSPSARCOPIHRCENOGIVEAAPGTQSD 207
 QY 181 TTCKNPLEPLPPMSGT 197
 DB 208 TTCKNPLEPLPPMSGT 224

RESULT 6
 ABP96136
 ID ABP96136 standard; protein; 399 AA.
 AC
 XX
 AC ABP96136;
 XX
 DT 09-MAY-2003 (first entry)
 XX
 DE Human TNF receptor 2 related protein variant SEQ ID NO.1.

XX
 KW Human; tumour necrosis factor receptor 2 related protein variant;
 KW TNFR2PV; cytosolic; immunosuppressive; antiasthmatic; gene therapy;
 KW TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;
 KW asthma; ulcerative colitis.
 XX
 OS Homo sapiens.
 XX
 PN W02003012037-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 24-JUL-2002; 2002MO-US023684.
 XX
 PR 27-JUL-2001; 2001US-00917372.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lal PG, Warren BA;
 XX WPI; 2003-256445/25.
 DR N-PSDB; ABZ79717.
 XX
 PT New CDNA, useful for preparing a composition for treating a disease or
 PT condition associated with increased TNF signaling e.g., cancer of the
 PT prostate, ovary, gallbladder, breast, brain, liver or colon, or
 PT rheumatoid arthritis, asthma.
 XX
 PS Claim 20; Fig 1A-F; 6app; English.
 XX
 CC The present sequence represents human tumour necrosis factor receptor 2
 CC related protein variant (TNFR2PV). TNFR2PV has cytosolic, antiasthmatic
 CC and immunosuppressive activities, and can be used in gene therapy. The
 CC TNFR2PV cDNA or protein sequences can be used for preparing a composition
 CC for treating a disease or condition associated with increased TNF
 CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,
 CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
 CC arthritis, asthma or ulcerative colitis
 CC
 XX
 SQ Sequence 399 AA;
 Query Match 99.6%; Score 1129; DB 6; Length 399;
 Best Local Similarity 99.5%; Pred. No. 4.3e-78;
 Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPQAVPYASBNQTCRDOEKERYEPQHRICCSRCPGGTVYSAKCSRIRDTVCATCAENS 60
 DB 28 SOPQAVPYASBNQTCRDOEKERYEPQHRICCSRCPGGTVYSAKCSRIRDTVCATCAENS 87
 QY 61 YNEHNNYLTICQLCRPCDPVWGLIEIAPCTSRKTKQCRQCPGMFCAAMALECTHCELLSD 120
 DB 88 YNEHNNYLTICQLCRPCDPVWGLIEIAPCTSRKTKQCRQCPGMFCAAMALECTHCELLSD 147
 QY 121 CEPGTAEIKDEVGKGNHNCVPCAKGHPONTSSPSARCOPIHRCENOGIVEAAPGTQSD 180
 DB 148 CEPGTAEIKDEVGKGNHNCVPCAKGHPONTSSPSARCOPIHRCENOGIVEAAPGTQSD 207
 QY 181 TTCKNPLEPLPPMSGT 197
 DB 208 TTCKNPLEPLPPMSGT 224

RESULT 7
 ADC42856
 ID ADC42856 standard; protein; 416 AA.
 AC
 XX
 AC ADC42856;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE RMAP protein #16.
 XX
 DE Cytostatic; Antiarteriosclerotic; Anti-HIV; Antiinflammatory;

KM Antiallergic; Antidiabetic; REMAP; pathogenesis.
XX OS Homo sapiens.
XX WO2003027228-A2.
XX PD 03-APR-2003.
XX PF 16-JUL-2002; 2002WO-US022833.
XX PR 17-JUL-2001; 2001US-0306020P.
PR 27-JUL-2001; 2001US-0308179P.
PR 02-AUG-2001; 2001US-0309702P.
PR 10-AUG-2001; 2001US-0311476P.
PR 10-AUG-2001; 2001US-0311551P.
PR 10-AUG-2001; 2001US-0311718P.
PR 24-AUG-2001; 2001US-0314798P.
PR 31-AUG-2001; 2001US-0316639P.
PR 07-SEP-2001; 2001US-0317996P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Lal PG, Honchell CD, Forsythe TJ, Walla NK, Tang TY, Borowsky ML;
PI Barroso I, Yue H, Warren BA, Thangavelu K, Gleitzen KJ, Azimzai Y;
PI Lee EA, Baughm MR, Gorvad AS, Duggan BM, Tran B, Li JX;
PI Richardson TW, Elliott VS, Zebardjian Y, Tran UK, Yao MG;
PI Peterson DP, Luo W, Lehr-Mason PM;
XX DR WPI; 2003-421156/39.
XX PT New human receptors and membrane-associated proteins (REMAP), useful for
PT diagnosing, treating or preventing disorders associated with aberrant
PT REMAP expression, e.g. cancer, AIDS, atherosclerosis, hypertension or
PT stroke.
XX PS Claim 1; SEQ ID NO 16; 115pp; English.
XX CC The present invention relates to an isolated polypeptide. The
XX CC polypeptides and polynucleotides are useful in diagnosing, treating and
XX CC preventing disorders associated with aberrant expression of REMAP, such
XX CC as cell proliferative, autoimmune/inflammatory, renal, neurological,
XX CC cardiovascular, metabolic, developmental, endocrine, muscle,
XX CC gastrointestinal, lipid metabolism or transport disorders, and viral
XX CC infections. These are also useful in assessing the effects of exogenous
XX CC compounds on the expression of nucleic acids and amino acid sequences of
XX CC REMAP, in facilitating drug discovery process, and in investigating the
XX CC pathogenesis of diseases or medical conditions. Expression and
XX CC purification were achieved using bacterial or virus-based expression
XX CC systems. The present sequence represents an REMAP protein of the
XX CC invention.
SQ Sequence 416 AA;
Query Match 97.8%; Score 1108; DB 7; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.8e-76;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 VPPASNNQCRDQEKYEYEPQHRICCSRCPPGTYSACSRIRIDVYCATCAENSYNEHM 65
DB 14 VPPASNNQCRDQEKYEYEPQHRICCSRCPPGTYSACSRIRIDVYCATCAENSYNEHM 73
QY 66 NYLTICQLCRPPCDPVMGLEIAPCTSKRTQRCQPGMFCAMALBCTHCELLSDCPGT 125
DB 74 NYLTICQLCRPPCDPVMGLEIAPCTSKRTQRCQPGMFCAMALBCTHCELLSDCPGT 133
QY 126 EAEIKDVGKGNHVCCKAGHPONTSSPSARCQPHTRCENQGLVEAAGTAQSDTTCKN 185
DB 134 EAEIKDVGKGNHVCCKAGHPONTSSPSARCQPHTRCENQGLVEAAGTAQSDTTCKN 193
QY 186 PLEPLPPEMSGT 197
DB 194 PLEPLPPEMSGT 205

RESULT 8
ID ADA49700
XX ADA49700 standard; protein; 170 AA.
XX AC ADA49700;
XX DT 20-NOV-2003 (first entry)
XX DE Extracellular region of human TNFRp (hTNFRp) protein.
XX KW Apo-2 ligand inhibitor; Apo-2L1; Apo-3; apoptosis; affinity;
XX competitive-type receptor; binding assay; cancer cell; human;
XX TNF receptor family; hTNFRp; cytosolic.
XX OS Homo sapiens.
XX PN US2002192729-A1.
XX PD 19-DEC-2002.
XX PE 28-MAR-2002; 2002US-00112793.
XX PR 01-APR-1996; 96US-00625328.
PR 23-SEP-1996; 96US-00710802.
PR 31-MAR-1997; 97US-00828683.
XX PA (GERTH) GENENTECH INC.
XX PI Ashkenazi AJ;
XX DR WPI; 2003-657226/62.
XX PT Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or
PT Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
XX in diagnostic assays.
XX PS Disclosure; Fig 2; 53pp; English.
XX CC The present invention relates to the isolation of a biologically active
XX CC Apo-2 ligand inhibitor (Apo-2L1) or Apo-3, and the polynucleotide
XX CC sequences encoding them. Apo-2L1 and Apo-3 are involved in apoptosis. The
XX CC Apo-2L1 and Apo-3 polypeptides are useful in diagnostic assays. Apo-2L1
XX CC is useful for generating antibodies, as standards in assays for Apo-3 or
XX CC Apo-2L1, in affinity purification techniques, and in competitive-type
XX CC receptor binding assays when labelled with radioiodine, enzymes or
XX CC fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or
XX CC inducing apoptosis in cancer cells, and thus have therapeutic utility.
XX CC The present sequence represents the extracellular region of a human TNF
XX CC receptor family protein. This sequence is compared with the extracellular
XX CC region of human Apo-2L1.
SQ Sequence 170 AA;
Query Match 87.1%; Score 987; DB 6; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-67;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TCBDQEKYEYEPQHRICCSRCPPGTYSACSRIRIDVYCATCAENSYNEHMYLTICQLC 74
DB 1 TCBDQEKYEYEPQHRICCSRCPPGTYSACSRIRIDVYCATCAENSYNEHMYLTICQLC 60
QY 75 RPQDPVMGLEIAPCTSKRTQRCQPGMFCAMALBCTHCELLSDCPGTAEIKDVEVG 134
DB 61 RPQDPVMGLEIAPCTSKRTQRCQPGMFCAMALBCTHCELLSDCPGTAEIKDVEVG 120
QY 135 KGNHVCCKAGHPONTSSPSARCQPHTRCENQGLVEAAGTAQSDTTCK 184
DB 121 KGNHVCCKAGHPONTSSPSARCQPHTRCENQGLVEAAGTAQSDTTCK 170
RESULT 9
AAB36700

ID AAB36700 standard; protein; 415 AA.
 XX
 AC AAB36700;
 XX
 DT 15-MAR-2001 (first entry)
 DE Human tumour necrosis factor receptor LTBR protein SEQ ID NO:6.
 XX
 KM Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TNF5; nototropic;
 KM TRAIL receptor without intracellular domain; diagnosis; cytostatic;
 KM tumour necrosis factor related apoptosis inducing ligand; vasotropic;
 KM immunosuppressive; neuroprotective; antiviral; antiinflammatory;
 KM anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
 KM gene therapy; restenosis; graft versus host disease; tumour; cancer;
 KM apoptotic cell death related disease; autoimmune disorder;
 KM cardiovascular disorder; viral infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200071150-A1.
 PD 30-NOV-2000.
 XX
 PF 18-MAY-2000; 2000WO-US013515.
 XX
 PR 20-MAY-1999; 99US-0135164P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Wei Y, Ruben SM, Gentz RL, Ni J;
 DR WPI; 2001-041051/05.
 XX
 PT Nucleic acid encoding a TRID polypeptide, also referred to as tumor
 PT necrosis factor receptor 5, useful in the diagnosis, treatment or
 PT prevention of cancer, autoimmune disorders and viral infection.
 XX
 PS Disclosure; Fig 2; 285pp; English.
 XX
 CC The present invention describes the human TRID protein (tumour necrosis
 CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
 CC intracellular domain, also referred to as tumour necrosis factor receptor
 CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nootropic,
 CC neuroprotective, antiviral, antiinflammatory, anticonvulsant,
 CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
 CC activities, and can be used in gene therapy. The TRID polynucleotides are
 CC useful for detecting complementary polynucleotides. TRID proteins and
 CC polynucleotides are useful in the treatment of tumours, resistance to
 CC parasite, bacteria and viruses, restenosis and graft versus host disease.
 CC They are also useful for inducing proliferation of T-cells, endothelial
 CC cells and certain hematopoietic cells, to regulate antiviral responses
 CC and to prevent certain autoimmune diseases after stimulation of TRID by
 CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
 CC polypeptides are useful for treating and/or preventing diseases
 CC associated with increased or decreased apoptotic cell death. The TRID
 CC polynucleotides, proteins, antibodies, agonists and antagonists are
 CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)
 CC autoimmune disorders; (c) diseases associated with increased apoptosis;
 CC (d) cardiovascular disorders; and (e) viral infection. The present
 CC sequence represents a tumour necrosis factor receptor used in comparison
 CC with TRID in the exemplification of the present invention
 XX
 XX Sequence 415 AA;
 SQ
 Query Match 68.0%; Score 771; DB 4; Length 415;
 Best Local Similarity 70.7%; Pred. No. 8.4e-51;
 Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;
 QY 1 SOPQAVPYASSENQTCRDOEKYEYEPORIRICCSRCPPTGYTSAKSGRIRIDTYCATCAENS 60
 DB 28 SOPQAVPYPRINQTCWDDQKEYEPMHDVCCSRCPGBFVAVCSRSQDTVCKTCHPHNS 87
 QY 61 YNEHNMNLTITCQLCRPCDPVWGLBEIAPCTSKRKTKQCRQPGMFCAMALBCTHC--ELL 118

DB 88 YNEHNMNHLSTCCQCRDCDIYLGFEVAPCTSDKKAACRCQPGMSCYLLDNECVHCEERL 147
 QY 119 SDCEPPTGEARLAKVEYAGKNNHCYPCKAGRHQONTSSPSARCQPHTRCNOGLVEAPCTAQ 178
 DB 148 VLCQPGTEAEVTDDEIMDTDVNCVPCPKGHPQNTSSPRARCQPHTRCEIQGLVEAPRTSY 207
 QY 179 SDTTCNNPLEP 189
 DB 208 SDTTCNNPPPP 218
 RESULT 10
 ABB96138
 ID ABB96138 standard; protein; 415 AA.
 XX
 AC ABB96138;
 XX
 DT 09-MAY-2003 (first entry)
 DE Mouse lymphotoxin-beta receptor protein SEQ ID NO:20.
 XX
 KM Human; tumour necrosis factor receptor 2 related protein variant;
 KM TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;
 KM TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;
 KM asthma; ulcerative colitis.
 XX
 OS Mus musculus.
 XX
 PN WO2003012037-A2.
 PD 13-FEB-2003.
 XX
 PF 24-JUL-2002; 2002WO-US023684.
 XX
 PR 27-JUL-2001; 2001US-00917372.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 PI Lal PG, Warren BA;
 DR WPI; 2003-256445/25.
 XX
 PT New cDNA, useful for preparing a composition for treating a disease or
 PT condition associated with increased TNF signaling e.g., cancer of the
 PT prostate, ovary, gallbladder, breast, brain, liver or colon, or
 PT rheumatoid arthritis, asthma.
 XX
 PS Disclosure; Fig 2A-C; 64pp; English.
 XX
 CC The present invention describes human tumour necrosis factor receptor 2
 CC related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic
 CC and immunosuppressive activities, and can be used in gene therapy. The
 CC TNFR2PV cDNA or protein sequences can be used for preparing a composition
 CC for treating a disease or condition associated with increased TNF
 CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,
 CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
 CC arthritis, asthma or ulcerative colitis. The present sequence represents
 CC a mouse lymphotoxin-beta receptor amino acid sequence, which is given in
 CC comparison with human TNFR2PV in the exemplification of the present
 CC invention
 XX
 XX Sequence 415 AA;
 SQ
 Query Match 68.0%; Score 771; DB 6; Length 415;
 Best Local Similarity 70.7%; Pred. No. 8.4e-51;
 Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;
 QY 1 SOPQAVPYASSENQTCRDOEKYEYEPORIRICCSRCPPTGYTSAKSGRIRIDTYCATCAENS 60
 DB 28 SOPQAVPYPRINQTCWDDQKEYEPMHDVCCSRCPGBFVAVCSRSQDTVCKTCHPHNS 87
 QY 61 YNEHNMNLTITCQLCRPCDPVWGLBEIAPCTSKRKTKQCRQPGMFCAMALBCTHC--ELL 118

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Db      88 YNEHWNHLSTCQLRCPDVIYGFEEVAPRSDRAKRCQCGMGCYVILNDCVACEERL 147
Oy      119 SDCCPTEAEILKDEYKGNHNCVCKKXGHFONTSPPARCOPTHRCENOGILVEAPGTAQ 178
Db      148 VLCQPGTEAEYTDIMTDVNCVPCRGHFONTSSPPARCOPTHRCIQLVEAPGTSY 207
Oy      179 SDTTCNNPDEP 189
Db      208 SDTTCNNPDEP 218

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RESULT 11
AAM94642
ID AAM94642 standard; peptide; 77 AA.
XX

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AC AAM94642;
XX
DT 29-APR-1999 (first entry)
XX
DE TNF-R extracellular Cys-rich domain TNF-R-1p.
XX
KW Tumour necrosis factor receptor; TNF-R; autoimmune diseases;
KW inflammation; septic shock; cachexia; graft versus host disease;
KW skin allergic reaction; immune complex disease; malaria;
KW transplantation rejection.
XX
OS Homo sapiens.
XX
PN WO9853842-A1.
XX
PD 03-DEC-1998.
XX
PE 29-MAY-1998; 98WO-US010691.
XX
PR 30-MAY-1997; 97US-00866545.
XX
PA (VYPE-) UNIV PENNSYLVANIA.
XX
PI Greene MI, Murali R, Takasaki W;
XX
DR WPI; 1999-080781/07.
XX

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```

PT New compounds designed from a binding loop of a tumour necrosis factor
PT receptor - are capable of inhibiting the biological activities of tumour
PT necrosis factor, e.g., in treating inflammation or autoimmune diseases.
XX
PS Disclosure; Fig 1; 78pp; English.
XX
CC The present invention describes peptides and peptide analogues which
CC correspond in primary sequence to a binding loop of a tumour necrosis
CC factor receptor (TNF-R) superfamily member. The compounds are especially
CC designed from a binding loop of TNF-R p55. They are capable of inhibiting
CC TNF binding to its cellular receptors and may be used to inhibit the
CC biological activities of TNF. They may be used in treating TNF-associated
CC conditions such as acute and chronic inflammatory responses, septic
CC shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic
CC reactions, immune complex disease, transplantation rejection and malaria.
CC Administration is, e.g. oral, transdermal, transmucosal, pulmonary,
CC subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5
CC mg/kg/day. The present sequence represents an extracellular Cys-rich
CC domain of TNF-R from the present invention
XX
SQ Sequence 77 AA;

```

```

Query Match 40.2%; Score 456; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.5e-27;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      52 VCATCAENSYNHNNYLTICQLCRPCDPMGLIEIAPCTSKRTQCRQCPGMFCAAMALE 111
Db      1 VCATCAENSYNHNNYLTICQLCRPCDPMGLIEIAPCTSKRTQCRQCPGMFCAAMALE 60

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```

Oy      112 CTHCELLSDCPPGTEAE 128
Db      61 CTHCELLSDCPPGTEAE 77

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RESULT 12
AAB69194
ID AAB69194 standard; protein; 77 AA.
XX
AC AAB69194;
XX
DT 30-APR-2001 (first entry)
XX
DE Human TNF-R extracellular Cys-rich domain TNF-R-1p SEQ ID NO:3.
XX

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```

KW Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;
KW osteoclastogenesis; bone loss; bone resorption; osteopathic; cytoskeletal;
KW antirheumatic; antiarthritic; antiinflammatory; immunomodulatory;
KW tumour necrosis factor-related activation-induced cytokine; TRANCE;
KW receptor activator of NF-kappa B ligand; RANK; osteoporosis;
KW Paget's disease; metastatic bone disease; rheumatoid arthritis;
KW periodontal disease; modulating dendritic cell maturation;
KW T cell proliferation; CD40 receptor system.
XX
OS Homo sapiens.
XX
PN WO200108699-A1.
XX
PD 08-FEB-2001.
XX
PE 28-JUL-2000; 2000WO-US020510.
XX
PR 28-JUL-1999; 99US-0146090P.
XX
PA (VYPE-) UNIV PENNSYLVANIA.
PA (AOKI/) AOKI K.
PA (HORN/) HORNE W C.
PA (BARO/) BARON R.
XX
PI Aoki K, Horne WC, Baron R, Greene MI, Murali R;
XX
DR WPI; 2001-182866/18.
XX

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```

PT Use of peptides and peptide analogs which are TRANCE/RANK inhibitors, for
PT inhibiting osteoclastogenesis and bone resorption.
XX
PS Disclosure; Fig 1; 81pp; English.
XX
CC The present invention describes a method for inhibiting
CC osteoclastogenesis and bone resorption. Osteoclastogenesis and bone
CC resorption inhibiting peptide analogues from the present invention have
CC osteopathic, cytoskeletal, antirheumatic, antiarthritic, antiinflammatory
CC and immunomodulatory activities, and are tumour necrosis factor (TNF)-
CC related activation-induced cytokine (TRANCE)/receptor activator of NF-
CC kappa B ligand (RANK) inhibitors. The method is useful for treating
CC diseases characterised by bone loss such as osteoporosis, Paget's
CC disease, metastatic bone disease, rheumatoid arthritis or periodontal
CC disease, and modulating dendritic cell maturation, T cell proliferation,
CC and/or CD40 receptor systems. The present sequence represents an
CC extracellular Cys-rich domain of a tumour necrosis factor receptor (TNF-
CC R) superfamily member, which is used in the exemplification of the
CC present invention
XX
SQ Sequence 77 AA;

```

```

Query Match 40.2%; Score 456; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.5e-27;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      52 VCATCAENSYNHNNYLTICQLCRPCDPMGLIEIAPCTSKRTQCRQCPGMFCAAMALE 111
Db      1 VCATCAENSYNHNNYLTICQLCRPCDPMGLIEIAPCTSKRTQCRQCPGMFCAAMALE 60

```

QY 112 CTCELLSDCPPGTAE 128
 |||||
 DB 61 CTCELLSDCPPGTAE 77

RESULT 13
 ABP41926 standard; protein; 305 AA.
 XX ABP41926;
 XX
 XX 22-AUG-2002 (first entry)
 DE Human ovarian antigen HSAB44, SEQ ID NO:3058.

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 ovarian cancer; breast cancer; tumour; reproductive system disorder;
 infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 inflammatory condition; immune disorder; blood disorder;
 cardiovascular disorder; respiratory disorder; neurological disorder;
 gastrointestinal disorder; urinary system disorder; drug screening;
 gene therapy; chromosome mapping; forensic analysis;
 antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 antiinflammatory; gynaecological; reproductive; chromosome 12p13.

XX Homo sapiens.
 OS
 XX WO200200677-A1.
 XX
 XX 03-JAN-2002.
 PD
 XX 07-JUN-2001; 2001WO-US018569.
 PP
 XX 07-JUN-2000; 2000US-0209467P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX (HUMA-) HUMAN GENOME SCI INC.
 PI
 XX Birse CE, Rosen CA;
 P1
 DR WPI; 2002-147878/19.
 DR N-PSDB; ABQ55003.

Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 cancer), immune disorders, cardiovascular disorders and neurological
 diseases.

Claim 11; SEQ ID NO 3058; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-
 ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 encompasses polypeptides 90% identical and polynucleotides 95% identical
 to the sequences of the invention. The invention additionally relates to
 recombinant vectors and host cells comprising human ovarian antigen and
 polynucleotides, antibodies against human ovarian antigens, and the use
 of ovarian antigen polynucleotides and polypeptides in diagnosing,
 treating, prognosing or preventing various ovary and/or breast-related
 disorders. Such conditions include ovarian cancer and breast cancer, and
 metastatic tumours of ovarian or breast origin, reproductive system
 disorders (e.g., infertility, disorders of pregnancy, anovulation,
 polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 vaginitis), immune disorders (e.g., congenital and acquired
 immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 blood-related disorders (e.g., anaemia), cardiovascular disorders,
 respiratory disorders, neurological disorders, gastrointestinal disorders
 and urinary system disorders. Ovarian antigen polypeptides and
 polynucleotides may also be used in screening for compounds which
 modulate ovarian antigen expression or activity. The polynucleotides may
 further be used for gene therapy, chromosome mapping, in the
 identification of individuals and in forensic analysis, and the

CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences
 XX

SO Sequence 305 AA:

QY 123 PGTEA-ELKDEVGKNNHCVPCKAGHFQNTSSPSARCCOPHTRCENOGIVEAAPGTASDST 181
 |||||
 DB 19 PGMPAFLLPDBVGGKNNHCVPCKRAGHFQNTSSPSARCCOPHTRCENOGIVEAAPGTASDST 78
 |||||

QY 182 TCKNPLEPLPEMSGT 197
 |||||
 DB 79 TCKNPLEPLPEMSGT 94
 |||||

RESULT 14
 AAR51003 standard; protein; 518 AA.
 XX AAR51003;
 XX
 XX 25-MAR-2003 (revised)
 DT 07-OCT-1994 (first entry)
 DT
 XX Sequence of a recombinant human (rhv) tumour necrosis factor receptor
 DE TNFR/FC fusion protein.
 DE
 XX Tumour necrosis factor receptor; chimeric antibody molecule;
 KW
 KW immunoglobulin.
 KW
 OS Synthetic.
 OS
 XX WO9406476-A1.
 XX
 XX 31-MAR-1994.
 PD
 XX 14-SEP-1993; 93WO-US008666.
 PP
 XX 15-SEP-1992; 92US-00946236.
 PR
 XX (IMMV) IMMUNEX CORP.
 PA
 XX Smith CA, Jacobs CA;
 PI
 XX WPI; 1994-118172/14.
 DR N-PSDB; AAQ45225.

Treating TNF mediated inflammatory diseases with TNF antagonist - esp.
 PT soluble form of TNF receptor, opt. as fusion protein with human
 PT immunoglobulin Fc region, esp. for treating arthritis.
 XX
 XX Disclosure: Page 32-34; 47pp; English.

AAQ45224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast
 cell line WI-26 VA4. The mature full-length TNFR1 is a glycoprotein
 CC having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for TNFR1
 CC was described in Smith et al., Science 248:1019,1990. Clone 1 is
 CC contained in expression vector pCAV/NOT-TNFR (ATCC 68088). A recombinant
 CC chimeric antibody may be produced having TNFR sequences substituted for
 CC the variable domains of either or both of the immunoglobulin molecule
 CC heavy and light chains and having unmodified constant region domains. A
 CC specific example of a TNFR/FC fusion protein is given in AAQ45225/R51003.
 CC The rhv TNFR/FC fusion gene was created by ligating the following
 CC fragments into a cloning vector: 1) an 867 bp Asp718-Pvu2 fragment from
 CC pCAV/NOT-TNFR (ATCC 68088) contg. the cDNA encoding the truncated TNFR.
 CC 2) a 700 bp StyI-SpeI fragment from plasmid pIX498 coding for 232 AAs of

CC the Fc portion of human IgG1. Plasmid pIXy498 is a yeast expression
CC vector contg. the Fc fragment of human IgG1. 3) An oligo linker, to fuse
CC the truncated TMFR with the human IgG1 Fc fragment. This linker was
CC created by PCR using primer AAQ45226, which encodes the 3' end of the
CC truncated TMFR receptor and the 5' end of human IgG1, and primer AAQ45227,
CC which is an antisense sequence encoding bps 257-257 of human IgG1.
CC (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ

Sequence 518 AA;

Query Match 27.8%; Score 315; DB 2; Length 518;

Best Local Similarity 35.5%; Pred. No. 5.9e-16; Mismatches 77; Indels 28; Gaps 9;

Matches 71; Conservative 24; Mismatches 77; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTCRDEKEYEPQHRICGSRCPGTVSAKSRIRDTVCATCAENSYNE 63
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 57 AFPPYAPBPSTGR--LRHYDQTAQMCCKSCSGQAKAFCTTSTVCDSCDSYTYQ 114
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 64 HNNYLTTCQLCR--PCDPYMGLEETAPCTSKRTQCRQCPMGFCAAMALE-CTHCELLS 119
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 115 LMMWVPECLSCGSRCSQYV---ETQACTREQNRICTCRPGWCALSKQBGCRICAPLR 170
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 120 DCPRG-----TEAELKDEYVGKNNHCYPCAKGHQNTSSPSARCOPTHRCENQGVYAAAP 174
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 171 KCRPFGVAPRGTTSDV-----CKPCAPGTFSTSTSDICRPHQICN---VVAIP 220
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 175 GTAQSDTTC--KNPLEPLPP 192
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 221 GNASMDAVCTSTSPTRSMAP 240
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 15

ABJ37103 ID ABJ37103 standard; protein; 659 AA.

XX AC ABJ37103;

XX DT 08-MAY-2003 (first entry)

XX DE Concatameric immunoadhesion human protein sequence SBQ ID No 12.

KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW dimeric protein; inflammation; septicemia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation; human.

XX OS Homo sapiens.

XX PN W02003010202-A1.

XX PD 06-FEB-2003.

XX PF 26-JUL-2002; 2002WO-KR001427.

XX PR 26-JUL-2001; 2001KR-00045028.

XX PA (MEDE-) MEDEXGEN CO LTD.

XX PI Chung Y, Han J, Lee H, Choi E, Kim J;

XX DR WPI, 2003-229639/22.

XX DR N-FSDB; ABJ32046.

PT New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.

XX Claim 27; Page 148-152; 211pp; English.

XX The invention relates to a novel concatameric protein comprising two
CC soluble domains, in which an N-terminus of a soluble domain of a
CC biologically active protein is linked to a C-terminus of an identical

CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammatory
CC related diseases. This sequence represents the human concatameric protein
CC of the invention
XX
SQ

Sequence 659 AA;

Query Match 27.5%; Score 311.5; DB 6; Length 659;

Best Local Similarity 36.4%; Pred. No. 1.4e-15; Mismatches 74; Indels 27; Gaps 9;

Matches 71; Conservative 23; Mismatches 74; Indels 27; Gaps 9;

QY 5 AVPPYASE-NQTCRDEKEYEPQHRICGSRCPGTVSAKSRIRDTVCATCAENSYNE 63
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 28 AFPPYAPBPSTGR--LRHYDQTAQMCCKSCSGQAKAFCTTSTVCDSCDSYTYQ 85
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 64 HNNYLTTCQLCR--PCDPYMGLEETAPCTSKRTQCRQCPMGFCAAMALE-CTHCELLS 119
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 86 LMMWVPECLSCGSRCSQYV---ETQACTREQNRICTCRPGWCALSKQBGCRICAPLR 141
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 120 DCPRG-----TEAELKDEYVGKNNHCYPCAKGHQNTSSPSARCOPTHRCENQGVYAAAP 174
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 142 KCRPFGVAPRGTTSDV-----CKPCAPGTFSTSTSDICRPHQICN---VVAIP 191
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 175 GTAQSDTTCCKNPLEP 189
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 192 GNASMDANCTSP-EP 205
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Search completed: August 28, 2004, 01:47:03
Job time : 129 secs

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OM protein - protein search, using SW model

Run on: August 28, 2004, 01:43:28 ; Search time 40 Seconds

(without alignments)
473.743 Million cell updates/sec

Title: US-10-003-211-1

Perfect score: 1133
Sequence: 1 SQPQAVPPYASENQCRDQF.....QSDTTCKNPLEPLPEPMSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 1133 | 100.0 | 435 | 2 | tumor necrosis fac |
| 2 | 1005 | 26.9 | 461 | 1 | tumor necrosis fac |
| 3 | 295 | 26.0 | 474 | 2 | tumor necrosis fac |
| 4 | 290 | 25.6 | 459 | 2 | gene murine tumor |
| 5 | 278 | 24.5 | 277 | 2 | B-cell activation |
| 6 | 243.5 | 21.5 | 305 | 2 | B-cell-associated |
| 7 | 226.5 | 20.0 | 651 | 2 | death receptor-6 - |
| 8 | 222.5 | 19.6 | 271 | 2 | OX40 antigen precu |
| 9 | 214.5 | 18.9 | 272 | 2 | gene OX40 protein |
| 10 | 210.5 | 18.6 | 455 | 1 | tumor necrosis fac |
| 11 | 210 | 18.5 | 348 | 2 | hypothetical prote |
| 12 | 210 | 18.5 | 349 | 2 | gene G4R protein - |
| 13 | 207 | 18.3 | 439 | 2 | G2R protein - vari |
| 14 | 206 | 18.2 | 461 | 2 | tumor necrosis fac |
| 15 | 201 | 17.7 | 277 | 2 | OX40 homolog - hum |
| 16 | 201 | 17.7 | 454 | 1 | tumor necrosis fac |
| 17 | 196 | 17.3 | 595 | 2 | CD30 antigen precu |
| 18 | 195.5 | 17.3 | 255 | 2 | lymphocyte activat |
| 19 | 189 | 16.7 | 325 | 2 | T2 protein - rabbi |
| 20 | 187.5 | 16.5 | 314 | 2 | FAS soluble protei |
| 21 | 184.5 | 16.3 | 461 | 1 | tumor necrosis fac |
| 22 | 183.5 | 16.2 | 326 | 1 | T2 protein - myxom |
| 23 | 181 | 16.0 | 335 | 2 | apoptosis-mediatin |
| 24 | 179.5 | 15.8 | 256 | 2 | T-cell antigen 4-1 |
| 25 | 171.5 | 15.1 | 425 | 1 | nerve growth facto |
| 26 | 166 | 14.7 | 493 | 2 | membrane glycoprot |
| 27 | 164 | 14.5 | 416 | 1 | nerve growth facto |
| 28 | 162 | 14.3 | 327 | 2 | apoptosis-mediatin |
| 29 | 148.5 | 13.1 | 427 | 1 | nerve growth facto |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 30 | 145.5 | 12.8 | 324 | 2 | JC2395 | Fas antigen precu |
| 31 | 133 | 11.7 | 260 | 1 | A46517 | CD27 antigen precu |
| 32 | 132.5 | 11.7 | 1111 | 2 | T26972 | hypothetical prote |
| 33 | 129.5 | 11.4 | 1620 | 2 | T27283 | hypothetical prote |
| 34 | 129 | 11.4 | 3084 | 1 | MMMSA | laminin alpha-1 ch |
| 35 | 128.5 | 11.3 | 1299 | 2 | T43251 | turin (EC 3.4.21.7 |
| 36 | 128 | 11.3 | 1274 | 2 | T42017 | cyteine rich prot |
| 37 | 126 | 11.1 | 3635 | 2 | T10053 | laminin alpha 5 ch |
| 38 | 125.5 | 11.1 | 2180 | 2 | T29764 | hypothetical prote |
| 39 | 124.5 | 11.0 | 899 | 2 | G02428 | subtilisin-like pr |
| 40 | 124.5 | 11.0 | 915 | 2 | JC6148 | subtilisin-like pr |
| 41 | 124.5 | 11.0 | 3707 | 2 | S18252 | heparan sulfate pr |
| 42 | 124 | 10.9 | 1680 | 2 | A43434 | turin (EC 3.4.21.7 |
| 43 | 123.5 | 10.9 | 686 | 2 | JC7569 | Delta-4 protein - |
| 44 | 123 | 10.9 | 722 | 2 | I48324 | DELTA-like 1 - mou |
| 45 | 122.5 | 10.8 | 915 | 1 | A48225 | subtilisin-like pr |

ALIGNMENTS

RESULT 1

154182 tumor necrosis factor receptor 2-related protein - human

C/Species: Homo sapiens (man)

C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000

C/Accession: 154182

R/Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.

A/Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequ

A/Reference number: 154182; MUID:93252381; PMID:8486360

A/Accession: 154182

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-435 <RSS>

A/Cross-references: GB:L04270; NID:G339761; PIDN:AAA36757.1; PID:G339762

C/Genetics:

A/Gene: GDB:LTBR

A/Cross-references: GDB:1230195; OMIM:600979

A/Map position: 12p13.3-12p13.1

C/Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 100.0%; Score 1133; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | SQPQAVPPYASENQTGRDQFKEYRPHRRICCSRCPGTYVSACSRIRDTVCATCAENS | 60 |
| DB | 28 | SQPQAVPPYASENQTGRDQFKEYRPHRRICCSRCPGTYVSACSRIRDTVCATCAENS | 87 |
| QY | 61 | YNEHWNYLTITICQLCRPCDPVWGLEIAPCTSKRTQRCQPGMFCAMALBECTHCELLSD | 120 |
| DB | 88 | YNEHWNYLTITICQLCRPCDPVWGLEIAPCTSKRTQRCQPGMFCAMALBECTHCELLSD | 147 |
| QY | 121 | CPPTGEALKDVEKGNHCVCKAHPONTSPSARCOPTRENOGLVEAPGTAQSD | 180 |
| DB | 148 | CPPTGEALKDVEKGNHCVCKAHPONTSPSARCOPTRENOGLVEAPGTAQSD | 207 |
| QY | 181 | TTCKNPLEPLPEPMSGT 197 | |
| DB | 208 | TTCKNPLEPLPEPMSGT 224 | |

RESULT 2

A35356 tumor necrosis factor receptor 2 precursor [validated] - human

N/Alternate names: 75X tumor necrosis factor receptor; TNF receptor type 2

C/Species: Homo sapiens (man)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 27-Oct-2003

C/Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094

R/Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S

Science 248: 1019-1023, 1999
A/Title: A receptor for tumor necrosis factor defines an unusual family of cellular an

A:Reference number: A35356; MUID:90260639; PMID:2160731
 A:Accession: A35356
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <SMI>
 A:Cross-references: GB:M2315; NID:g189185; PIDN:AAA59929.1; PID:g189186
 R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
 A:Reference number: A36475; MUID:91045991; PMID:2172983
 A:Accession: A36475
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-195; 'R', 197-461 <KOH>
 A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA5755.1; PID:g339758
 R:Dembl, Z.; Loeschner, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Genz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
 A:Reference number: A48416; MUID:91370690; PMID:1966549
 A:Accession: A48416
 A:Status: preliminary
 A:Molecule type: mRNA, protein
 A:Residues: 23-461 <DEM>
 A:Cross-references: GB:S63368; NID:g235648; PIDN:AA19824.1; PID:g235649
 A:Note: Sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)
 R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
 A:Reference number: A36007; MUID:90349572; PMID:2166946
 A:Accession: A36007
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 116-140; 'P', 142-195; 'R', 197-362; 'T', 364-461 <HEL>
 A:Cross-references: GB:M55857; NID:g339751; PIDN:AA63262.1; PID:g339752
 R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
 A:Reference number: A23666; MUID:91056048; PMID:2173696
 A:Accession: A23666
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-40; 65-69; 136-141; 300-306 <IOE>
 R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A:Reference number: A35010; MUID:90110215; PMID:2153136
 A:Accession: B35010
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-31 <ENG>
 R:Kuhnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
 A:Reference number: I38094; MUID:95121934; PMID:7821811
 A:Accession: I38094
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-37 <RES>
 A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
 A:Gene: GDB:TNFR2
 A:Cross-references: GDB:125914; OMIM:191191
 A:Map position: 1p36.2-1p36.2
 A:Introns: 26/3
 A:Note: The list of introns is incomplete
 C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
 F:40-76/Domain: NGF receptor repeat homology <NG3>
 F:78-119/Domain: NGF receptor repeat homology <NG3>
 F:120-162/Domain: NGF receptor repeat homology <NG3>
 F:164-201/Domain: NGF receptor repeat homology <NG4>

F:262-279/Domain: transmembrane #status predicted <TMN>
 F:280-461/Domain: intracellular #status predicted <INT>
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 26.9%; Score 305; DB 1; Length 461;
 Best Local Similarity 35.0%; Pred. No. 6,1e-16;
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
 QY 5 AVPPYASE-NOTGCDQEKYEPQHRICCSNCPPTGYASAKCSIRIDVVCATCAENSYNE 63
 DB 28 APTPYADEPGSTCR--LREYDDQTAQWCCSKSCSPQAKVFCYKSDVCDSCEDSTYQ 85
 QY 64 HMYVLTICQLCR---PCDPVWGLEIAPCTSKRTQCRQCPGMCAWALR-CTHCELLS 119
 DB 86 LMWVPECLSGSGSCSSDQV---ETQACTHEQNRICRCRGWCAIALSKQSGCRLCAPLR 141
 QY 120 DCPPG-----TEALKDEVGKGNHCVPKAGHFQNTSSPARCQPHTRCENQGLVEAP 174
 DB 142 KCRPGFVARPGTETSDV-----CKPCAGTFSNTTSTYDICRPHQICN---VVAIP 191
 QY 175 GTAOSDTTC--KNPLEPLPP 192
 DB 192 GNAAMDVACTSTSPTRMAP 211
 RESULT 3
 B38634
 tumor necrosis factor receptor type 2 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 27-Oct-2003
 C:Accession: B38634; A40254; S54816
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
 A:Reference number: A38634; MUID:91187885; PMID:1849278
 A:Accession: B38634
 A:Molecule type: mRNA
 A:Residues: 1-474 <LEM>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen Mol. Cell. Biol. 11, 3020-3026, 1991
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
 A:Reference number: A40254; MUID:91246168; PMID:1645445
 A:Accession: A40254
 A:Molecule type: mRNA
 A:Residues: 1-474 <GOO>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Kissonerghis, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor.
 A:Reference number: S54816
 A:Accession: S54816
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <RIS>
 A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA0618.1; PID:g809044
 C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homo.
 C:Keywords: cytochrome; signal sequence #status predicted <SIG>
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F:40-77/Domain: NGF receptor repeat homology <NG3>
 F:79-120/Domain: NGF receptor repeat homology <NG3>
 F:166-203/Domain: NGF receptor repeat homology <NG4>
 Query Match 26.0%; Score 295; DB 2; Length 474;
 Best Local Similarity 34.0%; Pred. No. 3,5e-15;
 Matches 66; Conservative 24; Mismatches 84; Indels 20; Gaps 8;
 QY 8 PYASE-NOTCRDQEKYEPQHRICCSNCPPTGYASAKCSIRIDVVCATCAENSYNEHN 66
 DB 31 FYKPEPGYECQISQ--FYIRKAKQMCACPKPPQGVHFCNKSIDTYCADCEASMYQWNN 89
 QY 67 YLTICQLCR---PCDPVWGLEIAPCTSKRTQCRQCPGMCA--AWALECTHCELLSDC 121

Db 90 QPRTLSGSSSTTTQV---ETRACTKQNNRVCACEBGRYALKTHTSGSCQCRRLSKC 145
 QY 122 PGTAEALKEVGVKGNHCVPCAKGHFQNTSSPSARCCQPHTECENQGLVEAPGTAOSDT 181
 Db 146 GGGF-GVASSRAPNGNVLCKACAPGTFSTTSSITVCPHRLCS---ILAIIPGNASTDA 200
 QY 182 TCKNPLEBPLPPEMS 195
 Db 201 VC---APESTPLTS 210

RESULT 4

148854

gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 27-Oct-2003
 C/Accession: 148854
 R/Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
 Mamm. Genome 5: 726-727, 1994
 A/Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
 A/Reference number: 148854; MUID:95178848; PMID:7873884
 A/Accession: 148854
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-459 <RES>
 A/Cross-references: EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:9433831
 C/Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
 F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 25.6%; Score 290; DB 2; Length 459;
 Best Local Similarity 33.5%; Pred. No. 8.2e-15;
 Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;

QY 8 PYASE-NQTRDQKEYEYPQHRICSRCPGTIVSAKSRIRDTVCATCAENSYNHN 66
 Db 16 PYKPEPEYEQISQ-EYDKRAQMCCKAPPGQYVAFCKNTSSTVCADCEASMTDVMN 74
 QY 67 YLTTCQLCR--PCDPVWGLEBIAPTCSKRTQCRCPGMFCA--AWALRCTHCELLSDC 121
 Db 75 QPRTLSGSSSTTTQV---ETRACTKQNNRVCACEBGRYALKTHTSGSCQCRRLSKC 130
 QY 122 PGTAEALKEVGVKGNHCVPCAKGHFQNTSSPSARCCQPHTECENQGLVEAPGTAOSDT 181
 Db 131 GGGF-GVASSRAPNGNVLCKACAPGTFSTTSSITVCPHRLCS---ILAIIPGNASTDA 185
 QY 182 TCKNPLEBPLPPEMS 195
 Db 186 VC---APESTPLTS 195

RESULT 5

A60771

B-cell activation protein CD40 precursor - human
 N/Alternate names: B-cell surface antigen Bp50
 C/Species: Homo sapiens (man)
 C/Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 C/Accession: S04460; A60771
 R/Stamenkovic, I.; Clark, E.A.; Seed, B.
 EMBO J. 8, 1403-1410, 1989
 A/Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
 A/Reference number: S04460; MUID:89356608; PMID:2475341
 A/Accession: S04460
 A/Molecule type: mRNA
 A/Residues: 1-277 <STA>
 A/Cross-references: EMBL:X60592; NID:929850; PIDN:CAA43045.1; PID:929851
 R/Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A/Title: Biochemical characteristics and partial amino acid sequence of the receptor-11k
 C/Comment: For an alternative splice form, see PIR:A46476.
 A/Reference number: A60771; MUID:89093941; PMID:2463309
 A/Accession: A60771
 A/Molecule type: protein
 A/Residues: 21-50 <BRA>

A/Experimental source: Burkitt lymphoma cell line Raji
 C/Genetics:
 A/Gene: GDB:CD40
 A/Cross-references: GDB:215268; OMIM:109335
 A/Map position: 20q12-20q13.2
 C/Superfamily: CD27 antigen; NGF receptor repeat homology
 C/Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prote
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-27/Product: B-cell activation protein CD40 #status experimental <MAT>
 F:21-193/Domain: extracellular #status predicted <EXT>
 F:194-215/Domain: transmembrane #status predicted <TM>
 F:216-277/Domain: intracellular #status predicted <CYT>
 F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.5%; Score 278; DB 2; Length 277;
 Best Local Similarity 35.0%; Pred. No. 4.4e-14;
 Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

QY 7 PYASENQTRDQKEYEYPQHRICSRCPGTIVSAKSRIRDTVCATCAENSYNHN 66
 Db 22 PPTA-----CR-EKQYLINSQ--CSLQCGQGLVSTCTFTETCLPCGESEFLDWN 72
 QY 67 YLTTCQLCRPCDPVWGLEBIAPTCSKRTQCRCPGMFCAWALECTHCELLSDCPGTE 126
 Db 73 RETHCHQHXCDPMLGLRVQKGTSEDTTICTCEGHNCTSEA--CSCVLHRCSPGPG 130
 QY 127 AELEKEVGVKGNHCVPCAKGHFQNTSSPSARCCQPHTECENQGLVEAPGTAOSDTTC 183
 Db 131 VK-QIANGVSDTICEPCVPGFSSVSAFKECHWTSCTETKDLVQQAQTKTIDVVC 186

RESULT 6

A46476

B cell-associated surface molecule CD40, long splice form - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
 C/Accession: A46476; A46515
 R/Torres, R.M.; Clark, E.A.
 J. Immunol. 148, 620-626, 1992
 A/Title: Differential increase of an alternatively polyadenylated mRNA species of mur
 A/Reference number: A46476; MUID:92105763; PMID:1370315
 A/Accession: A46476
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-305 <TOR>
 A/Cross-references: GB:M83312; NID:91553058
 A/Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIPI:75207)
 A/Note: this translation is not annotated in Genbank entry M83CD40A, release 113.0
 R/Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayn
 J. Immunol. 149, 3921-3926, 1992
 A/Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
 A/Reference number: A46515; MUID:93094586; PMID:1281194
 A/Accession: A46515
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-287, 'LV' <GR>
 A/Cross-references: GB:M83312; NID:91553058; PIDN:AB08705.1; PID:91553059; GB:M94126;
 A/Experimental source: BALB/c liver
 A/Note: sequence extracted from NCBI backbone (NCBIPI:120357)
 C/Comment: For an alternative splice form, see PIR:A46515.
 C/Comment: For an alternative splice form, see PIR:A46476.
 C/Superfamily: CD27 antigen; NGF receptor repeat homology
 C/Keywords: alternative splicing; transmembrane protein
 F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 21.5%; Score 243.5; DB 2; Length 305;
 Best Local Similarity 31.0%; Pred. No. 1.9e-11;
 Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;

QY 15 TCRDQKEYEYPQHRICSRCPGTIVSAKSRIRDTVCATCAENSYNHNVLTTCQLC 74
 Db 25 TCSD-KQYLHDGQ--CCDLQPGSRRLTSHCTALBKTCQHPDSCGFFSAQMNREIRCHQ 80

Query Match 75 RCPDPMGLEETAPCTSKKKTCCRCOPGMCAMALBCTHCELLSDCPG-----TEAFL 129
 Best Local Similarity 32.1%; Pred. No. 6.7e-10;
 Matches 53; Conservative 17; Mismatches 68; Indels 27; Gaps 5;
 Db 81 RICEPNOGIRVKKKEGAEEDTVCCKEGHCT--SKDCBAQAQHTCICIGFVMEWATEL 138
 QY 130 KDEVGKNNHCVPCKAGHFQNTSSPSARCOPIHRCENOGIYEAAPGASDPTTC 183
 Db 139 TDTV-----CHPCPVGFPSNOSLFEKCYPMTSCEDKNLEVLQKGTSTNVIC 186

RESULT 7

JC7705
 death receptor-6 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 07-Jul-2003
 C:Accession: JC7705
 R:Brigdenham, J.T.; Bohe, J.; Goetz, F.W.; Johnson, A.L.
 Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
 A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.
 A:Reference number: JC7705; MUID:21308433; PMID:11414698
 A:Accession: JC7705
 A:Molecule type: mRNA
 A:Residues: 1-651 <BRI>
 A:Cross-references: GB:AF349908
 C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNF receptor superfamily, a cell death and/or survival signaling cascade.
 C:Genetics:
 A:Gene: dr-6
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: signal sequence #status predicted <SIG>
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
 F:332-350/Domain: transmembrane #status predicted <TM>
 F:410-475/Domain: death domain #status predicted <DED>
 F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 20.0%; Score 226.5; DB 2; Length 651;
 Best Local Similarity 28.8%; Pred. No. 6.5e-10;
 Matches 49; Conservative 26; Mismatches 62; Indels 33; Gaps 6;

QY 30 ICSCRPGTGVSAKCSIRDTVCATCAENSYNEHNNYLTICQLCR-PCDPMGLEETAP 88
 Db 50 LICKCPAGTYVSKKCTSTRECSPPCDGFTTKENGIERCHPRKKE--LPILKETH 107
 QY 89 CTSKKTCCRCOPGMF-----CAAMALBCTHCELLSDCP-----PSTELKDEVGK 136
 Db 108 CTALDRECTCLSGFQINDICVPTV-----CPVGWVARKKGETE----- 149
 QY 137 NNHCVPCKAGHFQNTSSPSARCOPIHRCENOGIYEAAPGASDPTTC 186
 Db 150 DVRCAPCLRGTFSDVPSVWCKCTYTDGCKNMVYVVKPTKESDNCXSP 199

RESULT 8

S12783
 OX40 antigen precursor - rat
 N:Alternate names: nerve growth factor receptor homology
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: S12783; S08036
 R:Mallett, S.; Fossum, S.; Barclay, A.N.
 EMBO J. 9, 1063-1068, 1990
 A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes
 A:Reference number: S12783; MUID:90214614; PMID:2157591
 A:Accession: S12783
 A:Molecule type: mRNA
 A:Residues: 1-271 <MAL>

A:Cross-references: EMBL:X17037; NID:957830; PIDN:CA34897.1; PID:957831
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: growth factor receptor; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-271/Product: OX40 antigen #status predicted <MAT>
 F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 19.6%; Score 222.5; DB 2; Length 271;
 Best Local Similarity 32.1%; Pred. No. 6.7e-10;
 Matches 53; Conservative 17; Mismatches 68; Indels 27; Gaps 5;

QY 21 KEYEPORHICSRCPPTGVSAKCSIRDTVCATCAENSYNEHNNYLTICQLCRPCDPV 80
 Db 28 KDTYPSGHR-CCRECPGHWVSRCDTRDTVCHPEPEGYNAVYDT-CQCTCCNHR 85
 QY 81 MGLEETAPCTSKKKTCCRCOPGMCAMALBCTHCELLSDCPGTEAEIKDEVGKNNHC 140
 Db 86 SGEELKQNTCTPTEDTVCQCR-----PGTQPR-QDSGHRKGVDC 122
 QY 141 VPCKAGHFQNTSSPSARCOPIHRCENOGIYEAAPGASDPTTC 185
 Db 123 VPCPPHGFPSGNA--CKPWTNCTLSGKQIRHPSANSIDTVDCD 165

RESULT 9

gene OX40 protein - mouse
 N:Alternate names: OX40 antigen
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
 C:Accession: I48700; I48334; S34377
 R:Calderhead, D.M.; Buhlmann, J.E.; van den Bertwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993
 A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell interaction.
 A:Reference number: I48700; MUID:94044750; PMID:8228223
 A:Accession: I48700
 A:Status: translated from GB/EMBL/DBJ

A:Accession: I48700
 A:Molecule type: mRNA
 A:Residues: 1-272 <RES>
 A:Cross-references: EMBL:Z21674; NID:9312827; PIDN:CA49772.1; PID:9312828
 R:Brigdenham, J.T.; Bohe, J.; Goetz, F.W.; Johnson, A.L.
 Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
 A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.
 A:Reference number: I48334; MUID:95255413; PMID:7737295
 A:Accession: I48334
 A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-14, G, 16-272 <RE2>
 A:Cross-references: EMBL:X85214; NID:9732818; PIDN:CA59476.1; PID:9732819
 C:Genetics:
 A:Gene: ox40
 A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
 C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 18.9%; Score 214.5; DB 2; Length 272;
 Best Local Similarity 31.7%; Pred. No. 2.7e-09;
 Matches 53; Conservative 16; Mismatches 67; Indels 31; Gaps 6;

QY 21 KEYEPORHICSRCPPTGVSAKCSIRDTVCATCAENSYNEHNNYLTICQLCRPCDPV 80
 Db 29 KATYPSGHR-CCRECPGHWVSRCDTRDTVCHPEPEGYNAVYDT-CQCTCCNHR 86
 QY 81 MGLEETAPCTSKKKTCCRCOPGMCAMALBCTHCELLSDCPGTEAEIKDEVGKNNHC 140
 Db 87 SGEELKQNTCTPTEDTVCQCR-----PGTQPR-QDSGHRKGVDC 123
 QY 141 VPCKAGHFQNTSSPSARCOPIHRCENOGIYEAAPGASDPTTC 185
 Db 124 VPCPPHGF-----SPGNNOACKPWTNCTLSGKQIRHPSANSIDTVDCD 166

RESULT 10

GOHUT1
 tumor necrosis factor receptor 1 precursor [validated] - human
 N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
 C:Accession: A38208; A34899; A34900; A35555; C36555; A38281; S12057; U70758; A60231; A
 R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F.

Genomics 13, 219-224, 1992
 A>Title: Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to chromosome 6
 A/Reference number: A38208; MUID:92250049; PMID:1315717
 A/Accession: A38208
 A/Molecule type: DNA
 A/Residues: 1-455 <LOC>
 A/Cross-references: GB:M5864; GB:M75865; GB:M75866; NID:G339748; PIDN:AAA61201.1; PID:G339748; R/Letscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, C.; Cell 61, 351-359, 1990
 A/Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor
 A/Reference number: A34899; MUID:90235284; PMID:2158862
 A/Accession: A34899
 A/Molecule type: mRNA
 A/Residues: 1-455 <LOC>
 A/Cross-references: GB:M58286; GB:M33480; NID:G339753; PIDN:AAA6753.1; PID:G339754
 A/Experimental source: Placenta
 A/Note: Part of this sequence, including the amino end of the mature protein, confirmed by S1/S2/S3/S4/S5/S6/S7/S8/S9/S10/S11/S12/S13/S14/S15/S16/S17/S18/S19/S20/S21/S22/S23/S24/S25/S26/S27/S28/S29/S30/S31/S32/S33/S34/S35/S36/S37/S38/S39/S40/S41/S42/S43/S44/S45/S46/S47/S48/S49/S50/S51/S52/S53/S54/S55/S56/S57/S58/S59/S60/S61/S62/S63/S64/S65/S66/S67/S68/S69/S70/S71/S72/S73/S74/S75/S76/S77/S78/S79/S80/S81/S82/S83/S84/S85/S86/S87/S88/S89/S90/S91/S92/S93/S94/S95/S96/S97/S98/S99/S100/S101/S102/S103/S104/S105/S106/S107/S108/S109/S110/S111/S112/S113/S114/S115/S116/S117/S118/S119/S120/S121/S122/S123/S124/S125/S126/S127/S128/S129/S130/S131/S132/S133/S134/S135/S136/S137/S138/S139/S140/S141/S142/S143/S144/S145/S146/S147/S148/S149/S150/S151/S152/S153/S154/S155/S156/S157/S158/S159/S160/S161/S162/S163/S164/S165/S166/S167/S168/S169/S170/S171/S172/S173/S174/S175/S176/S177/S178/S179/S180/S181/S182/S183/S184/S185/S186/S187/S188/S189/S190/S191/S192/S193/S194/S195/S196/S197/S198/S199/S200/S201/S202/S203/S204/S205/S206/S207/S208/S209/S210/S211/S212/S213/S214/S215/S216/S217/S218/S219/S220/S221/S222/S223/S224/S225/S226/S227/S228/S229/S230/S231/S232/S233/S234/S235/S236/S237/S238/S239/S240/S241/S242/S243/S244/S245/S246/S247/S248/S249/S250/S251/S252/S253/S254/S255/S256/S257/S258/S259/S260/S261/S262/S263/S264/S265/S266/S267/S268/S269/S270/S271/S272/S273/S274/S275/S276/S277/S278/S279/S280/S281/S282/S283/S284/S285/S286/S287/S288/S289/S290/S291/S292/S293/S294/S295/S296/S297/S298/S299/S300/S301/S302/S303/S304/S305/S306/S307/S308/S309/S310/S311/S312/S313/S314/S315/S316/S317/S318/S319/S320/S321/S322/S323/S324/S325/S326/S327/S328/S329/S330/S331/S332/S333/S334/S335/S336/S337/S338/S339/S340/S341/S342/S343/S344/S345/S346/S347/S348/S349/S350/S351/S352/S353/S354/S355/S356/S357/S358/S359/S360/S361/S362/S363/S364/S365/S366/S367/S368/S369/S370/S371/S372/S373/S374/S375/S376/S377/S378/S379/S380/S381/S382/S383/S384/S385/S386/S387/S388/S389/S390/S391/S392/S393/S394/S395/S396/S397/S398/S399/S400/S401/S402/S403/S404/S405/S406/S407/S408/S409/S410/S411/S412/S413/S414/S415/S416/S417/S418/S419/S420/S421/S422/S423/S424/S425/S426/S427/S428/S429/S430/S431/S432/S433/S434/S435/S436/S437/S438/S439/S440/S441/S442/S443/S444/S445/S446/S447/S448/S449/S450/S451/S452/S453/S454/S455/S456/S457/S458/S459/S460/S461/S462/S463/S464/S465/S466/S467/S468/S469/S470/S471/S472/S473/S474/S475/S476/S477/S478/S479/S480/S481/S482/S483/S484/S485/S486/S487/S488/S489/S490/S491/S492/S493/S494/S495/S496/S497/S498/S499/S500/S501/S502/S503/S504/S505/S506/S507/S508/S509/S510/S511/S512/S513/S514/S515/S516/S517/S518/S519/S520/S521/S522/S523/S524/S525/S526/S527/S528/S529/S530/S531/S532/S533/S534/S535/S536/S537/S538/S539/S540/S541/S542/S543/S544/S545/S546/S547/S548/S549/S550/S551/S552/S553/S554/S555/S556/S557/S558/S559/S560/S561/S562/S563/S564/S565/S566/S567/S568/S569/S570/S571/S572/S573/S574/S575/S576/S577/S578/S579/S580/S581/S582/S583/S584/S585/S586/S587/S588/S589/S590/S591/S592/S593/S594/S595/S596/S597/S598/S599/S600/S601/S602/S603/S604/S605/S606/S607/S608/S609/S610/S611/S612/S613/S614/S615/S616/S617/S618/S619/S620/S621/S622/S623/S624/S625/S626/S627/S628/S629/S630/S631/S632/S633/S634/S635/S636/S637/S638/S639/S640/S641/S642/S643/S644/S645/S646/S647/S648/S649/S650/S651/S652/S653/S654/S655/S656/S657/S658/S659/S660/S661/S662/S663/S664/S665/S666/S667/S668/S669/S670/S671/S672/S673/S674/S675/S676/S677/S678/S679/S680/S681/S682/S683/S684/S685/S686/S687/S688/S689/S690/S691/S692/S693/S694/S695/S696/S697/S698/S699/S700/S701/S702/S703/S704/S705/S706/S707/S708/S709/S710/S711/S712/S713/S714/S715/S716/S717/S718/S719/S720/S721/S722/S723/S724/S725/S726/S727/S728/S729/S730/S731/S732/S733/S734/S735/S736/S737/S738/S739/S740/S741/S742/S743/S744/S745/S746/S747/S748/S749/S750/S751/S752/S753/S754/S755/S756/S757/S758/S759/S760/S761/S762/S763/S764/S765/S766/S767/S768/S769/S770/S771/S772/S773/S774/S775/S776/S777/S778/S779/S780/S781/S782/S783/S784/S785/S786/S787/S788/S789/S790/S791/S792/S793/S794/S795/S796/S797/S798/S799/S800/S801/S802/S803/S804/S805/S806/S807/S808/S809/S810/S811/S812/S813/S814/S815/S816/S817/S818/S819/S820/S821/S822/S823/S824/S825/S826/S827/S828/S829/S830/S831/S832/S833/S834/S835/S836/S837/S838/S839/S840/S841/S842/S843/S844/S845/S846/S847/S848/S849/S850/S851/S852/S853/S854/S855/S856/S857/S858/S859/S860/S861/S862/S863/S864/S865/S866/S867/S868/S869/S870/S871/S872/S873/S874/S875/S876/S877/S878/S879/S880/S881/S882/S883/S884/S885/S886/S887/S888/S889/S890/S891/S892/S893/S894/S895/S896/S897/S898/S899/S900/S901/S902/S903/S904/S905/S906/S907/S908/S909/S910/S911/S912/S913/S914/S915/S916/S917/S918/S919/S920/S921/S922/S923/S924/S925/S926/S927/S928/S929/S930/S931/S932/S933/S934/S935/S936/S937/S938/S939/S940/S941/S942/S943/S944/S945/S946/S947/S948/S949/S950/S951/S952/S953/S954/S955/S956/S957/S958/S959/S960/S961/S962/S963/S964/S965/S966/S967/S968/S969/S970/S971/S972/S973/S974/S975/S976/S977/S978/S979/S980/S981/S982/S983/S984/S985/S986/S987/S988/S989/S990/S991/S992/S993/S994/S995/S996/S997/S998/S999/S1000/S1001/S1002/S1003/S1004/S1005/S1006/S1007/S1008/S1009/S1010/S1011/S1012/S1013/S1014/S1015/S1016/S1017/S1018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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2004, 01:33:14 ; Search time 25 Seconds

(without alignments)
410.313 Million cell updates/sec

Title: US-10-003-211-1

Perfect score: 1133

Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTCKNPLEPPPEMNGT 197

Scoring table:

BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | # Query | Length | ID | Description |
|------------|-------|---------|--------|----|-------------|
| 1 | 1133 | 100.0 | 435 | 1 | TNR3_HUMAN |
| 2 | 771 | 68.0 | 415 | 1 | TNR3_MOUSE |
| 3 | 305 | 26.9 | 461 | 1 | TR1B_HUMAN |
| 4 | 295 | 26.0 | 474 | 1 | TR1B_MOUSE |
| 5 | 285.5 | 25.2 | 300 | 1 | TR6B_HUMAN |
| 6 | 283 | 25.0 | 625 | 1 | TR1I_MOUSE |
| 7 | 278 | 24.5 | 277 | 1 | TNR5_HUMAN |
| 8 | 277 | 24.4 | 616 | 1 | TR1I_HUMAN |
| 9 | 251.5 | 22.2 | 269 | 1 | TNR5_BOVIN |
| 10 | 243.5 | 21.5 | 289 | 1 | TNR5_MOUSE |
| 11 | 242.5 | 21.4 | 401 | 1 | T11B_MOUSE |
| 12 | 239.5 | 21.1 | 401 | 1 | T11B_HUMAN |
| 13 | 235.5 | 20.8 | 401 | 1 | T11B_MOUSE |
| 14 | 230.5 | 20.3 | 283 | 1 | T11B_RAT |
| 15 | 228.5 | 20.2 | 655 | 1 | TR14_HUMAN |
| 16 | 226.5 | 20.0 | 655 | 1 | TR21_HUMAN |
| 17 | 225 | 19.9 | 655 | 1 | TR21_MOUSE |
| 18 | 222.5 | 19.6 | 349 | 1 | CRMB_CAMPS |
| 19 | 214.5 | 18.9 | 272 | 1 | TNR4_RAT |
| 20 | 210.5 | 18.6 | 455 | 1 | TNR4_MOUSE |
| 21 | 210 | 18.5 | 349 | 1 | CRMB_HUMAN |
| 22 | 207 | 18.3 | 351 | 1 | CRMB_MOUSE |
| 23 | 206 | 18.2 | 461 | 1 | TR1A_PIG |
| 24 | 203 | 17.9 | 333 | 1 | TNR6_BOVIN |
| 25 | 201 | 17.7 | 277 | 1 | TNR4_HUMAN |
| 26 | 201 | 17.7 | 454 | 1 | TR1A_HUMAN |
| 27 | 196 | 17.3 | 595 | 1 | TNR8_MOUSE |
| 28 | 195.5 | 17.3 | 255 | 1 | TNR9_HUMAN |
| 29 | 194 | 17.1 | 332 | 1 | TNR6_PIG |
| 30 | 189 | 16.7 | 325 | 1 | VT2_SFVKA |
| 31 | 188 | 16.6 | 471 | 1 | TR1A_BOVIN |
| 32 | 184.5 | 16.3 | 461 | 1 | TR1A_RAT |
| 33 | 183.5 | 16.2 | 326 | 1 | VT2_MYXVL |

| | | | | | | |
|----|-------|------|-----|---|------------|---------------------|
| 34 | 182 | 16.1 | 498 | 1 | TNR8_MOUSE | Q60846 mus musculus |
| 35 | 181 | 16.0 | 335 | 1 | TNR6_HUMAN | P25445 homo sapien |
| 36 | 179.5 | 15.8 | 256 | 1 | TNR9_MOUSE | P20334 mus musculus |
| 37 | 171.5 | 15.1 | 425 | 1 | TR16_RAT | P07174 rattus norv |
| 38 | 167.5 | 14.8 | 440 | 1 | T10B_HUMAN | 014763 homo sapien |
| 39 | 166 | 14.7 | 493 | 1 | TNR8_RAT | P97525 rattus norv |
| 40 | 164 | 14.5 | 416 | 1 | TR16_CHICK | P18519 gallus gall |
| 41 | 162 | 14.3 | 327 | 1 | TNR6_MOUSE | P25446 mus musculus |
| 42 | 152.5 | 13.5 | 417 | 1 | TR16_MOUSE | Q92041 mus musculus |
| 43 | 148.5 | 13.1 | 427 | 1 | TR16_HUMAN | P08138 homo sapien |
| 44 | 145.5 | 12.8 | 324 | 1 | TNR6_RAT | Q63199 rattus norv |
| 45 | 145 | 12.8 | 198 | 1 | TR22_MOUSE | Q6r62 mus musculus |

ALIGNMENTS

RESULT 1
TNR3_HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
DE protein) (Tumor necrosis factor C receptor).
GN LTRR OR TNFRSF3 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=93253381; PubMed=8486360;
RX Baens M., Chaffanet M., Cassiman J.-J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human 12P
RT transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=22388257; PubMed=12477932;
RX Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lottelino N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Botterfield Y.S.N., Krzyzanski M.T., Skalska U.,
RA Schnerke A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., VanAartsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfeld B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
[4]
RP CHARACTERIZATION.

RX MEDLINE=99223511; PubMed=10207006;
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
 RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
 RT death in HeLa cells".
 RL J. Biol. Chem. 274:11868-11873 (1999).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=20261554; PubMed=10799510;
 RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
 RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
 RT "The lymphotoxin-beta receptor is necessary and sufficient for
 RT LIGHT-mediated apoptosis of tumor cells".
 RL J. Biol. Chem. 275:14307-14315 (2000).
 RN [6]
 RP INTERACTION WITH TRAF3.
 RX MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 RA Yagita H., Okumura K.;
 RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
 RT the lymphotoxin-beta receptor".
 RL J. Biol. Chem. 271:14661-14664 (1996).
 RN [7]
 RP INTERACTION WITH TRAF4.
 RX MEDLINE=98289299; PubMed=9626059;
 RA Krajewska M., Krajewski S., Zapata J.M., VanAntsdale T.,
 RA Gascoyne R.D., Berern K., McFadden D., Shabalik A., Hugh J.,
 RA Reynolds A., Cleverger C.V., Reed J.C.;
 RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
 RT adult, fetal, and tumor tissues".
 RL Am. J. Pathol. 152:1549-1561 (1998).
 RN [8]
 RP INTERACTION WITH TRAF5.
 RX MEDLINE=98172745; PubMed=9511754;
 RA Muzushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
 RA Otsuka M., Yamamoto T., Inoue J.-I.;
 RT "Cloning and characterization of a cDNA encoding the human homolog of
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5)".
 RL Gene 207:135-140 (1998).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTb, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs.
 CC -1- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
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 CC -----
 CC EMBL: L04270; AAA36757.1; -;
 DR EMBL: BC026262; AAH26262.1; -;
 DR PIR: I54182; I54182.
 DR HSSP: P25942; 1CDF.
 DR Genem: HGNC:6718; LTBR.
 DR MIM: 600979; -;
 DR GO: GO:0007165; P:signal transduction; TNS.
 DR InterPro: IPR008063; Fas_receptor.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR PRINTS: PR01680; FASRECEPTOR.
 DR SMART: SM00208; TNFR. 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00650; TNFR_NGFR_2; 3.
 DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 30
 FT CHAIN 1 435
 FT TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPERFAMILY MEMBER 3.
 FT DOMAIN 31 227
 FT TRANSMEM 228 248
 FT POTENTIAL.
 FT EXTRACELLULAR (POTENTIAL).
 FT

FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 42 81 TNFR-CYS 1.
 FT REPEAT 82 124 TNFR-CYS 2.
 FT REPEAT 125 168 TNFR-CYS 3.
 FT REPEAT 169 211 TNFR-CYS 4.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 80 BY SIMILARITY.
 FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 139 148 BY SIMILARITY.
 FT DISULFID 142 167 BY SIMILARITY.
 FT DISULFID 170 185 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 435 AA; 46709 MW; 6246266022P656F CRC64;
 SQ
 Query Match 100.0%; Score 1133; DB 1; Length 435;
 Best Local Similarity 100.0%; Pred. No. 9, 1e-90;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQQAVPPVASENQTCDQKEYEYEPQHRICSCRCPGTVYSAKCSRIPTVCATCAENS 60
 Db 28 SQQAVPPVASENQTCDQKEYEYEPQHRICSCRCPGTVYSAKCSRIPTVCATCAENS 87
 QY 61 YNEHWNYLTITCOLCRPCDPVWGLEETAPCTSKRTQCRQCPGMCAWALECTHCELLSD 120
 Db 88 YNEHWNYLTITCOLCRPCDPVWGLEETAPCTSKRTQCRQCPGMCAWALECTHCELLSD 147
 QY 121 CPPTGEAELEKDEVGKNNHCVPCKAGHFONTSSPSARCOPTRCENQGLVEAPGTQSD 180
 Db 148 CPPTGEAELEKDEVGKNNHCVPCKAGHFONTSSPSARCOPTRCENQGLVEAPGTQSD 207
 QY 181 TTCKNPPLPPPPENSGT 197
 Db 208 TTCKNPPLPPPPENSGT 224
 RESULT 2
 TNFR_MOUSE STANDARD; PRT; 415 AA.
 ID TNFR3_MOUSE
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (lymphotoxin-beta receptor).
 GN LTBR OR TNFRSF3 OR TNFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CVB; TISSUE=Lung;
 RX MEDLINE=96072804; PubMed=7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression".
 RL J. Immunol. 155:5280-5288 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Nakano T.;
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 RT sequence trap and chromosomal mapping".
 RL J. Genomics 30:312-319 (1995).
 RN [3]
 RP INTERACTION WITH TRAF5.
 RP


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Db 86 LMNWPBCLSCSSRSSDQV-----ETQACTRBNRITCGRPRWYALSKQSGCRICAPLR 141
QY 120 DCPG-----TEAEIKDEVGKGNHCVCKAGHPONTSSPSARCPHTRCENOGIVEAP 174
Db 142 KCRPGFVGARPGTETSDV-----CKPCAGTFTSNTSSDIDCRPHQICN-----VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
Db 192 GNASMDAVCTSTSPTRSMAP 211

RESULT 4
TRIB MOUSE
ID TRIB MOUSE STANDARD; PRT; 474 AA.
AC P2519; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (TNF-R2) (p75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.,
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific."
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor."
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=MOD;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RA Klesnerzhis M., Fellows R., Feldmann M., Chernajovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor with high affinity for TNFR2/TNF-alpha and
CC approximately 5-fold lower affinity for homotrimeric
CC TNFR1/Lymphotoxin-alpha. The TNFR1/TNFR2 complex recruits the
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (by
CC similarity).
CC -1- SUBUNIT: Binds to TNFR2 (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
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CC -----
CC EMBL; M60469; AAA39752.1; -
CC DR EMBL; M59378; AAA40463.1; -
CC DR EMBL; U39488; AAA85021.1; -

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DR EMBL; X87128; CAA60618.1; -.
DR PIR; B38634; B38634.
DR HSSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0008220; P:necrosis; IMP.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6_4.
DR SMART; SMO0208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT FT SIGNAL 1 22
FT CHAIN 23 474
FT FT DOMAIN 23 258 TUMOR NECROSIS FACTOR RECEPTOR
FT TRANSMEM 259 288 SUPERFAMILY MEMBER 1B.
FT DOMAIN 289 474 EXTRACELLULAR (POTENTIAL).
FT REPEAT 39 77 CYTOPLASMIC (POTENTIAL).
FT REPEAT 78 119 TNFR-CYS 1.
FT REPEAT 120 164 TNFR-CYS 2.
FT REPEAT 165 203 TNFR-CYS 3.
FT DISULFID 40 54 TNFR-CYS 4.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 26.0%; Score 295; DB 1; Length 474;
Best Local Similarity 34.0%; Pred. No 3.6e-18;
Matches 66; Conservative 24; Mismatches 84; Indels 20; Gaps 8;

QY 8 PYASE-NQTRDQEKYEYEPQHRICSRCPGTYVSACSRIRDPVATCATCAENSYNEHMN 66
Db 31 PYRDEGYEQISQ-EYEDKKAQMCACRPGYVGHFKKTSDDTVCADCEAMTYGVNM 89
QY 67 YLTICQLCR---PCDEYMGLEIAPCTSKRKTCCRCQPGMCA--AMALECHCEILSDC 121
Db 90 QFRTCSSSSCTTDYV---ETRACTKQDNRYCACEAGRYCALKTHSGSCRCOCMLSKC 145
QY 122 PGTEAEIKDEVGKGNHCVCKAGHPONTSSPSARCPHTRCENOGIVEAPGTAGSDPT 181
Db 146 GRPF-GVASSRANGVLCCKAARPGFTSSTIDVCRPRITCS-----IIAIFGNASTDA 200
QY 182 TCKNPLEPLPPENS 195
Db 201 VC-----APSSPTLS 210

RESULT 5
TRIB HUMAN
ID TRIB HUMAN STANDARD; PRT; 300 AA.
AC O95407;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
DE receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68).
GN TNFRSF6B OR DCR3 OR TR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal Lung;
 RX MEDLINE=99087326; PubMed=9872321;
 RA Pitti R.W., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
 RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
 RA Goddard A.D., Botstein D., Ashkenazi A.;
 RA "Genomic amplification of a decoy receptor for Fas ligand in lung and
 RT colon cancer";
 RL Nature 396:699-703(1998).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
 RC TISSUE=Prostate;
 RX MEDLINE=99253915; PubMed=10318773;
 RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
 RA "A newly identified member of tumor necrosis factor receptor
 RT superfamily (TR6) suppresses LIGHT-mediated apoptosis";
 RL J. Biol. Chem. 274:13733-13736(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=20122600; PubMed=10655513;
 RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
 RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
 RA "Overexpression of M68/DCR3 in human gastrointestinal tract tumors
 RT independent of gene amplification and its location in a four-gene
 RT cluster";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dichtenko L., Marutka K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran P.N.A., Peters G.J., Abramson R.D., Mullanb S.J.,
 RA Bosnak S., McGwen P.J., McKernan K.J., Malek J.A., Gamarallne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hallyk S.W.,
 RA Villalón D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RC -1- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF4/LIGHT
 and TNFSF6/FasL. Protects against apoptosis.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
 CC Detected in adult stomach, spinal cord, lymph node, trachea,
 CC spleen, colon and lung. Highly expressed in several primary tumors
 CC from colon, stomach, rectum, esophagus and in SW480 colon
 CC carcinoma cells.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
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CC EMBL: AF104419; RAD03056.1; -
 DR EMBL: AF134240; RAD29688.1; -
 DR EMBL: AF217796; AAF35244.1; -
 DR EMBL: AF217793; AAF33685.1; -
 DR EMBL: AF217794; AAF33686.1; -
 DR EMBL: AL121845; AAC03668.1; -
 DR EMBL: BC017065; AAH17065.1; -
 DR EMBL: BC034349; AAH34349.1; -
 DR HSSP: O14763; ID0G.
 DR Genew; HGNC:11921; TNFRSF6B.
 DR MIM: 603361; -
 DR GO: GO:0005625; C:soluble fraction; TAS.
 DR GO: GO:0008189; F:apoptosis inhibitor activity; TAS.
 DR GO: GO:0004872; F:receptor activity; TAS.
 DR GO: GO:0006916; F:anti-apoptosis; TAS.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR Receptor; Apoptosis; Glycoprotein; Repeat; signal.
 FW SIGNAL 1 29
 FT CHAIN 30 300
 FT REPEAT 31 70 TUMOR NECROSIS FACTOR RECEPTOR
 FT REPEAT 72 113 SUPERFAMILY MEMBER 6B.
 FT REPEAT 115 150 TNFR-CYS 1.
 FT REPEAT 152 193 TNFR-CYS 2.
 FT REPEAT 152 193 TNFR-CYS 3.
 FT REPEAT 152 193 TNFR-CYS 4.
 FT DISULFID 49 62 BY SIMILARITY.
 FT DISULFID 52 70 BY SIMILARITY.
 FT DISULFID 73 88 BY SIMILARITY.
 FT DISULFID 91 105 BY SIMILARITY.
 FT DISULFID 95 113 BY SIMILARITY.
 FT DISULFID 115 126 BY SIMILARITY.
 FT DISULFID 132 150 BY SIMILARITY.
 FT DISULFID 153 168 BY SIMILARITY.
 FT DISULFID 174 193 BY SIMILARITY.
 FT CARBOHYD 173 173 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 300 AA; 32679 MW; P0AEE3718449A6 CRC64;
 Query Match 25.2%; Score 285.5; DB 1; Length 300;
 Best Local Similarity 36.0%; Pred. No. 1.5e-17;
 Matches 63; Conservative 18; Mismatches 77; Indels 17; Gaps 7;
 QY 25 EPQRIICSRPPPGYVSAKSRIRDTVCATCAENSYMEHNVYLTICQLCPGCPVWG-- 82
 Db 42 ETGERLVCAQCPGTFVORPCRDSPTTCGCPPHHTQFNNYL--ERCRYCNVLCGER 98
 QY 83 LEEIAPCTSKRRTQRCQCPMFC--AAWALIECTHCEILSDCPGTEAEIKDEYKGNHCV 141
 Db 99 EEEARACIAITINRACRCRTGFPAHAGFCLR--H--ASCPGA-GVIAFGTPSQNTQCQ 151
 QY 142 PCKAGHPONTSSPSARCCPHTRCENQGLVEAPAGTADDTCKN----PIEPLPP 152
 Db 152 PCPPGTFASSSSSSPQCQPHRNCITAGIALNVPGSSSHDTICTSGTGPLSTRVP 206
 RESULT 6
 ID TR11 MOUSE STANDARD; PRT; 625 AA.
 AC 035305; Q8VCT7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11A precursor
 DE (Receptor activator of NF-kB) (Osteoclast differentiation factor
 DE receptor) (ODFR).
 GN TNFRSF11A OR RANK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;

[1]
 RN SEQUENCE FROM N.A.
 RP TISSUE: Fetal liver;
 RC MEDLINE=96032977; PubMed=9367155;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Douglall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Gajbert L.,
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE: Mammary gland;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mulhany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [3]
 RN FUNCTION.
 RP MEDLINE=96097247; PubMed=9678548;
 RA Nakagawa N., Kinoshita K., Yamaguchi K., Shima N., Yasuda H., Yano K.,
 RA Watanabe T., Higashio K.;
 RT "RANK is the essential signaling receptor for osteoclast
 RT differentiation factor in osteoclastogenesis";
 RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
 CC -1- FUNCTION: Receptor for TNFRSF11/RANKL/TRANCE/ODGL, essential for
 CC RANKL-mediated osteoclastogenesis. Involved in the regulation of
 CC interactions between T-cells and dendritic cells.
 CC -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
 CC TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
 CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, AF019046; AAB68610.1; -;
 DR EMBL, BC019185; AAH19185.1; -;
 DR HSSP, P25942; ICDF.
 DR MGD, MGI:1314891; Tnfrcfla.
 DR GO, GO:0007275; P:development; IMP.
 DR GO, GO:0007515; P:lymph gland development; IMP.
 DR InterPro: IPR001368; TNFR_c6.
 DR SMART, SM00208; TNFR_4.
 DR PROSITE, PS00652; TNFR_NGFR_1; 1.
 DR PROSITE, PS50050; TNFR_NGFR_2; 1.

KW Receptor, Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL
 FT CHAIN 1
 FT 31 625
 FT DOMAIN 31 214
 FT TRANSMEM 215 234
 FT DOMAIN 235 625
 FT REPEAT 35 69
 FT REPEAT 72 113
 FT REPEAT 115 152
 FT REPEAT 155 195
 FT REPEAT 35 47
 FT DISULFID 48 61
 FT DISULFID 51 69
 FT DISULFID 72 87
 FT DISULFID 93 113
 FT DISULFID 115 128
 FT DISULFID 134 152
 FT CARBOHYD 106 106
 FT CARBOHYD 175 175
 FT CONFLICT 494 494
 SQ SEQUENCE 625 AA; 66621 MW; P8C1872B9511DBE CRC64;
 Query Match 25.0%; Score 283; DB 1; Length 625;
 Best Local Similarity 32.6%; Pred. No. 5e-17;
 Matches 60; Conservative 25; Mismatches 85; Indels 14; Gaps 4;
 QY 4 QAVPYVASENQTCDQKEVEYEPHRIICSGCPGTVSAKCSIRITVCATCAENSYNE 63
 Db 30 QVTPPTCTOE-----RHVEHIGR-CCSCCEGKLSCTPTSSVCLPCGPDEYLD 79
 QY 64 HWNYITICOLCRPCDPVWGLEIEIAPCTSKRTQRCQPGMFCAMALECTCELSIDCEP 123
 Db 80 TWNEEDKCLHKYVDACKALVAVDPGNHTAPRACAGH--WNSDCECRNTECAP 136
 QY 124 GTEAEHLKDEYKGNHNCVPCKAGHFONTSSPSARQPHTRCENGLVEAPAGTAQSDPTTC 183
 Db 137 GFCAQHPLQLNK-DIVCTPCLIGFSDVFSSTDKCKPWTCTLLGKLEAHQGTTESDVVC 195
 QY 184 KNPI 187
 Db 196 SSSM 199
 RESULT 7
 TNRS HUMAN STANDARD; PRT; 277 AA.
 AC P25942; Q9BYU0;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, last sequence update)
 DT 15-MAR-2004 (Rel. 43, last annotation update)
 DE Tumor necrosis factor receptor superfamily member 5 precursor
 DE (CD40; receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).
 GN TNFRSF5 OR CD40.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM I).
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beate D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Graffam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.U., Heath P.D., Ho S., Holden J.L., Howden P.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Key M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Laveslaisho M.H., Laversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McMay K., Murray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "the DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:665-671(2001).
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM II).
 RX MEDLINE=2111710; PubMed=11172023;
 RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
 RT "Regulation of CD40 function by its isoforms generated through
 RT alternative splicing";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
 [4]
 RP SEQUENCE FROM N.A. (ISOFORM I).
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Mullany S.J.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany P.H.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.E., Sodergren E.D., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]
 RP INTERACTION WITH TRAF3.
 RX MEDLINE=95184010; PubMed=7533327;
 RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
 RT "Involvement of CRAF, a relative of TRAF, in CD40 signaling.";
 RL Science 267:1494-1498(1995).
 [6]
 RP INTERACTION WITH TRAF3.
 RX MEDLINE=95129692; PubMed=7530216;
 RA Sato T., Irie S., Reed J.C.;
 RT "A novel member of the TRAF family of putative signal transducing
 RT proteins binds to the cytosolic domain of CD40.";
 RL FEBS Lett. 358:113-118(1995).
 [7]
 RP INTERACTION WITH TRAF1, TRAF2, TRAF3 AND TRAF5.
 RX MEDLINE=98384149; PubMed=9718306;
 RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
 RA Kehy M.R.;
 RT "CD40-tumor necrosis factor receptor-associated factor (TRAF
 RT interactions: regulation of CD40 signaling through multiple TRAF

RT binding sites and TRAF hetero-oligomerization.";
 RL Biochemistry 37:11836-11845(1998).
 [8]
 RP INTERACTION WITH TRAF5.
 RX MEDLINE=98172745; PubMed=9511754;
 RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
 RA Otsuka M., Yamamoto T., Inoue J.-I.;
 RT "Cloning and characterization of a cDNA encoding the human homolog of
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
 RL Gene 207:135-140(1998).
 [9]
 RP INTERACTION WITH TRAF6.
 RX MEDLINE=9805703; PubMed=9432981;
 RA Kashiwada M., Shirakata Y., Inoue T.-I., Nakano H., Okazaki K.,
 RA Okumura K., Yamamoto T., Nagaoka H., Takemori T.;
 RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates
 RT extracellular signal-regulated kinase (ERK) activity in CD40
 RT signaling along a ras-independent pathway.";
 RL J. Exp. Med. 187:237-244(1998).
 [10]
 RP 3D-STRUCTURE MODELING OF 24-144.
 RX MEDLINE=97189482; PubMed=9037712;
 RA Bajorath J., Aruffo A.;
 RT "Construction and analysis of a detailed three-dimensional model of
 RT the ligand binding domain of the human B cell receptor CD40.";
 RL Proteins 27:59-70(1997).
 [11]
 RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
 RX MEDLINE=98266353; PubMed=9605317;
 RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
 RA Zheng Z., Naismith J.H., Thomas D.;
 RT "The role of polar interactions in the molecular recognition of CD40L
 RT with its receptor CD40.";
 RL Protein Sci. 7:1124-1135(1998).
 [12]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
 RP TRAF3.
 RX MEDLINE=20442386; PubMed=10984535;
 RA Ni C.Z., Welch K., Leo E., Chou C.K., Wu H., Reed J.C., Ely K.R.;
 RT "Molecular basis for CD40 signaling mediated by TRAF3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
 [13]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH
 RP TRAF3.
 RX MEDLINE=22000222; PubMed=12005438;
 RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,
 RA Satterthwaite A.C., Cheng G., Ely K.R.;
 RT "Downstream regulator TANK binds to the CD40 recognition site on
 RT TRAF3.";
 RL Structure 10:403-411(2002).
 [14]
 RP VARIANT H1GM3 ARG-83.
 RX MEDLINE=21532985; PubMed=11675497;
 RA Ferrari S., Gillani S., Insalaco A., Al-Ghonaum A., Sorsina A.R.,
 RA Loubser M., Avanzini M.A., Marconi M., Badolati R., Ugazio A.G.,
 RA Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D.,
 RA Plebani A.;
 RT "Mutations of CD40 gene cause an autosomal recessive form of
 RT immunodeficiency with hyper IgM.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
 [15]
 RP FUNCTION: Receptor for TNFSF5/CD40L.
 CC -1 SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein (isoform I);
 CC secreted (isoform II).
 CC -1 ALTERNATIVE PRODUCTS.
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=I;
 CC IsoId=P25942-1; Sequence=Displayed;
 CC Name=II;
 CC IsoId=P25942-2; Sequence=VSP_006472; VSP_006473;
 CC TISSUE SPECIFICITY: B-cells and in primary carcinomas.
 CC -1 DISEASE: Defects in TNFSF5 are the cause of hyper-IgM

CC immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an
 CC autosomal recessive disorder which includes an inability of B
 CC cells to undergo isotype switching, one of the final
 CC differentiation steps in the humoral immune system, an inability
 CC to mount an antibody-specific immune response, and a lack of
 CC germinal center formation.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
 CC -----
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 CC -----
 CC EMBL: X60592; CAA43045.1; -;
 CC EMBL: AL035662; CAC17670.1; -;
 CC EMBL: AJ300189; CAC29424.1; -;
 CC EMBL: BC012419; AAH12419.1; -;
 CC PIR: S04460; A60771.
 CC PDB: 1CDP; 01-APR-97.
 CC PDB: 1FLL; 18-OCT-00.
 CC PDB: 1LOA; 08-FEB-00.
 CC PDB; 1CZ2; 26-SEP-01.
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 CC Query Match 24.5%; Score 278; DB 1; Length 277;
 CC Best Local Similarity 35.0%; Pred. No. 6,1e-17;
 CC Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;
 CC
 CC QY 7 PYVASENOTCDEKYEYEPQHRICSRCPPTVYSAKSRIRDTVCATCAENSYEHWN 66
 CC Db 22 PPTA-----CR--EKQYLINSQ--CCSLCPQGLVSDCFEFTTECLPCGSESEFLDTWN 72
 CC QY 67 YLTICQACRPDPMGHEBETAPCSKRTQCRCPGFMCAAMALECHGELLSDCPGTE 126
 CC Db 73 RETHGHQKRYCDPMLGLRVQKQKSEDTDTCTCEBGMHCTSEA--CRSCVLRHSCSPGFG 130
 CC QY 127 AELKDEVGKNNHCVPCKAGHPONTSSPSARCPHTECGNGIVAEAPGASPTTC 163
 CC Db 131 VK-QIATGVSDTICPCPVGFFSVSAFKEKCHWTSCETKDLVQQAQNTKTDVVC 166
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 CC RESULT 8
 CC TR11 HUMAN STANDARD; PRT; 616 AA.
 CC ID TR11 HUMAN STANDARD; PRT; 616 AA.
 CC AC G9Y6G6;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Tumor necrosis factor receptor superfamily 11A precursor
 CC (Receptor activator of NF-kB) (osteoclast differentiation factor
 CC receptor) (ODPR)
 CC GN TNFRSF11A OR RANK.
 CC OS Homo sapiens (human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC OC NCBI_TaxId=9606;
 CC RN [1]
 CC RP SBOUENCE FROM N.A.
 CC RC TISSUE=Endritic cell;
 CC RA MEDLINE=98032977; PubMed=9367155;
 CC RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougal W.C.,
 CC RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 CC RA Galibert L.;
 CC RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 CC RT and dendritic-cell function.";
 CC RL Nature 390:175-179(1997).
 CC RN [2]
 CC RP FUNCTION.
 CC RX MEDLINE=99097247; PubMed=9878548;

RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
 RA Morinaga T., Higashio K.;
 RT "RANK is the essential signaling receptor for osteoclast
 RT differentiation factor in osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
 CC [3]
 CC INTERACTION WITH TRAF1, TRAF2, TRAF3, TRAF5 AND TRAF6.
 CC MEDLINE=98447691; PubMed=9774460;
 CC Wong B.R., Josien R., Lee S.Y., Vologodskaya M., Steiman R.M.,
 CC Choi Y.;
 CC "The TRAF family of signal transducers mediates NF-kappaB activation
 CC by the TRANCE receptor.";
 CC J. Biol. Chem. 273:28355-28359(1998).
 CC [4]
 CC VARIANT PEO LBU-LEU-CYS-ALA-LEU-LEU-21 INS, VARIANT PDB2
 CC ALA-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS, AND VARIANT VAL-192.
 CC MEDLINE=20082806; PubMed=10615125;
 CC Hughes A.E., Ralston S.H., Marken T., Bell C., Macpherson H.,
 CC Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
 CC Anderson D.M.;
 CC "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
 CC familial expansile osteolysis.";
 CC Nat. Genet. 24:45-48(2000).
 CC -1- FUNCTION: Receptor for TNFRSF11/RANKL/TRANCE/OPGL; essential for
 CC RANKL-mediated osteoclastogenesis. Involved in the regulation of
 CC interactions between T-cells and dendritic cells.
 CC -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Ubiquitous expression with high levels in
 CC skeletal muscle, thymus, liver, colon, small intestine and adrenal
 CC gland.
 CC -1- DISEASE: Defects in TNFRSF11A are the cause of familial expansile
 CC osteolysis (FEO) [MIM:174810]. FEO is a rare autosomal dominant
 CC bone disorder characterized by focal areas of increased bone
 CC remodeling. The osteolytic lesions develop usually in the long
 CC bones during early adulthood. FEO is often associated with early
 CC onset deafness and loss of dentition.
 CC -1- DISEASE: Defects in TNFRSF11A are a cause of Paget disease of bone
 CC 2 (PDB2) [MIM:602080]; also known as familial Paget disease of
 CC bone. PDB2 is a bone remodelling disorder with clinical
 CC similarities to FEO. Unlike FEO, however, affected individuals
 CC have involvement of the axial skeleton with lesions in the spine,
 CC pelvis and skull.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC
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 CC -----
 CC EMBL: AF018253; AAB86809.1; -;
 CC HSSP; P25942; 1CDF.
 CC DR Genew: HGNC:11908; TNFRSF11A.
 CC DR MIM; 603499; -;
 CC DR MIM; 174810; -;
 CC DR MIM; 602080; -;
 CC DR GO; GO:0004872; F:receptor activity; TAS.
 CC DR GO; GO:0007267; P:cell-cell signaling; TAS.
 CC DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 CC DR GO; GO:0007165; P:signal transduction; TAS.
 CC DR InterPro; IPR001358; TNFR_c6.
 CC DR Pfam; PF00020; TNFR_c6; 4.
 CC DR SMART; SM00208; TNFR; 4.
 CC DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 CC DR PROSITE; PS00652; TNFR_NGFR_2; 1.
 CC DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
 CC KW Disease mutation; Deafness.
 CC FT SIGNAL 1 29 POTENTIAL.
 CC FT CHAIN 30 616 TUMOR NECROSIS FACTOR RECEPTOR
 CC SUPERFAMILY MEMBER 11A.

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FT DOMAIN 30 212 EXTRACELLULAR (POTENTIAL).
FT TRASMEN 213 233 POTENTIAL.
FT DOMAIN 234 616 CYTOPLASMIC (POTENTIAL).
FT REPEAT 34 68 TNFR-CYS 1.
FT REPEAT 71 112 TNFR-CYS 2.
FT REPEAT 114 151 TNFR-CYS 3.
FT REPEAT 154 194 TNFR-CYS 4.
FT DISULFID 34 46 BY SIMILARITY.
FT DISULFID 47 60 BY SIMILARITY.
FT DISULFID 50 68 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 92 112 BY SIMILARITY.
FT DISULFID 114 127 BY SIMILARITY.
FT DISULFID 133 151 BY SIMILARITY.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 L-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 21 21 /FTID=VAR_011516.
FT VARIANT 21 21 L-> LALLCAL (in PDB2).
FT VARIANT 21 21 /FTID=VAR_011517.
FT VARIANT 21 21 A-> V.
FT VARIANT 192 192 /FTID=VAR_011518.
FT SEQUENCE 616 AA; 6603 MW; E3DE9A7A08196F81 CRC64;

Query Match 24.4%; Score 277; DB 1; Length 616;
Best Local Similarity 31.7%; Pred. No. 1,6e-16;
Matches 60; Conservative 28; Mismatches 87; Indels 14; Gaps 4;

QY 4 QANPPVASENOTCRDQKEYEPQHRICGSRCPGTVSASCRIRPTVCATCAENSUNE 63
DB 29 QIAPPCITSE-----KHEHLGR--CCNCKEFGKMTSMCTTSDSVCLPCGPDEYLD 78
QY 64 HNNVLTTCOLCRPDPVWGLEEIAPTCKRTQCRCPGMECAAMALECTHCELLSDCP 123
DB 79 SWNEEDKCLHKVCDTGKALVAAGNSTTPRCACCTGYA---MSODCECCRENTBCAP 135
QY 124 GTEAELEKDEVEKGNHCVPCAGHFOHTSSPSARCOPTHCENOGVLAAGTASDPTC 183
DB 136 GLGQHHPQLNKK-DTVCRCPLAGYFSDAFSSITDKCRPWTNCTFLGKRVHHGTEKSDAVC 194
QY 184 KNPIEPLPP 192
DB 195 SSSLPARKP 203

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RESULT 9
TNRS_BOVIN STANDARD; PRT; 269 AA.

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AC Q28203; 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (Fragment).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
OK NCBI_TaxID=9913;
RN SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Bates D.M.;
RT "Cloning, expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle.";
RT Immunology 90:294-300(1997).
CC -1- FUNCTION: Receptor for TNFRSF5/CD40L.
CC -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
CC similarity). LOCATION: Type I membrane protein.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.

```

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```

CC EMBL: U57745; AAC48710.1; -.
DR HSSP; P25942; 1CDP.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR01368; TNFR_c6.
DR Pfam; PF00020; TNFR_C6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
KW SIGNAL.
FT CHAIN 1 19
FT 20 >269
FT 20 193
FT 194 215
FT 216 >269
FT 225 60
FT 61 103
FT 104 144
FT 145 187
FT 187 37
FT 37 51
FT 51 59
FT 62 77
FT 77 103
FT 103 116
FT 116 119
FT 119 125
FT 125 143
FT 143 153
FT 153 180
FT 180 269
FT NON TER 269
SQ SEQUENCE 269 AA; 29983 MW; 746903F0F95F387 CRC64;

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Query Match 22.2%; Score 251.5; DB 1; Length 269;
 Best Local Similarity 33.1%; Pred. No. 1,1e-14;
 Matches 55; Conservative 21; Mismatches 81; Indels 9; Gaps 4;

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QY 20 EKEYEPQHRICGSRCPGTVSASCRIRPTVCATCAENSUNEHNNVLTTCOLCRPDP 79
DB 28 EKQY--PVNSLCCDLCFPGQKIVNDCTEVSKEQSCGKGFLSTWNEKCYCHEHRYCNP 85
QY 80 VNGLEEIAPTCKRTQCRCPGMECAAMALECTHCELLSDCPPTGEAELEKDEVGKG--N 137
DB 86 NIGLAIQSEGTLNTDTICVAVGGHCTSHT--CEBCTPHSLCLPFGYV--QIATGLLD 140
QY 138 NHCVPCKAGHFOHTSSPSARCOPTHCENOGVLAAGTASDPTC 183
DB 141 TVCEPCPLGFFSNVSSAFKCHRTSCERKGLVEQHVGNKTDVVC 186

```

RESULT 10
TNRS_MOUSE STANDARD; PRT; 289 AA.

```

AC P27512; Q99NE0; Q99NE1; Q99NE2; Q99NE3;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDW40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
OK NCBI_TaxID=10090;

```


RESULT 11
 TL1B MOUSE
 ID TL1B MOUSE STANDARD; PRT; 401 AA.
 AC 008712; 070202; 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11B precursor
 DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
 GN TNFRSF11B OR OPG OR OCIF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI TaxID=10090;
 [1]
 RP SOURCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Kidney;
 RX MEDLINE=97262071; PubMed=9104485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luehly R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy B., Bucy N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.U.;
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density.";
 RL Cell 89:309-319(1997).
 [2]
 RP SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
 RP AND ARG-296.
 RC STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
 RX MEDLINE=98382527; PubMed=9714833;
 RA Miuno A., Murakami A., Nakagami N., Yasuda H., Tsuda E., Morinaga T.,
 RA Higashio K.;
 RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
 RT gene and its expression in embryogenesis.";
 RL Gene 215:339-343(1998).
 [3]
 RP FUNCTION.
 RX MEDLINE=21060987; PubMed=10952716;
 RA Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
 RA Van G., Kaufman S., Kostenuik P.U., Lacey D.L., Boyle W.J.,
 RA Simonet W.S.;
 RT "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
 RT osteoclasts and prevents vascular calcification by blocking a process
 RT resembling osteoclastogenesis.";
 RL J. Exp. Med. 192:463-474(2000).
 [4]
 RL EXP. Med. 192:463-474(2000).
 CC -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
 CC its function in osteoclastogenesis. Inhibits the activation of
 CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
 CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
 CC play a role in preventing arterial calcification. May act as decoy
 CC receptor for TRAIL and protect against apoptosis. TRAIL binding
 CC blocks the inhibition of osteoclastogenesis.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
 CC intestines and calvaria. Highly expressed in decidua and placenta,
 CC and in embryo.
 CC -1- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
 CC whereas expression decreases at day 11 and increases from day 15
 CC to 17. On day 15 found in developing bone primordia,
 CC brachiocephalic artery and ductus arteriosus, left main bronchus,
 CC abdominal aorta and midgut.
 CC -1- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
 CC 1,25-dihydroxyvitamin D3 and parathyroid hormone.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 2 death domains.
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 CC -----
 CC EMBL; U94331; AAB53708.1; -;
 DR EMBL; AB013898; BAA28269.1; -;
 DR EMBL; AB013903; BAA33388.1; -;
 DR EMBL; AB013899; BAA33388.1; JOINED.
 DR EMBL; AB013900; BAA33388.1; JOINED.
 DR EMBL; AB013901; BAA33388.1; JOINED.
 DR EMBL; AB013902; BAA33388.1; JOINED.
 DR HSSP; P25942; ICDF.
 DR MGD; MGI:109587; Tnfisf11b.
 DR GO; GO:0005578; C:extracellular matrix; IDA.
 DR InterPro; IPR004488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS50017; DEATH DOMAIN; 1.
 DR PROSITE; PS50052; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
 FT SIGNAL 1
 FT CHAIN 22 401
 FT FT
 FT REPEAT 24 62
 FT REPEAT 65 105
 FT REPEAT 107 142
 FT REPEAT 145 185
 FT DOMAIN 198 269
 FT SITE 283 365
 FT SITE 400 400
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 107 118
 FT DISULFID 124 142
 FT DISULFID 145 160
 FT DISULFID 166 185
 FT CARBOHYD 98 98
 FT CARBOHYD 165 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT VARIANT 138 138
 FT VARIANT 161 161
 FT VARIANT 165 165
 FT VARIANT 288 288
 FT VARIANT 296 296
 FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;
 SQ
 Query Match 21.4%; Score 242.5; DB 1; Length 401;
 Best Local Similarity 29.6%; Pred. No. 9,4e-14;
 Matches 50; Conservative 25; Mismatches 83; Indels 11; Gaps 5;
 QY 23 YEPQ-RRICSRCPPTGVASAKSRIRDTVCATCAENSVMNMYLTICQLCR-CDP 79
 Db 30 HYDPGHLDDKAPGYLYLKQHCVRKRTLCVPCPDHSYDMSWTSDECVYCSVCKE 89
 QY 80 VNGLEIADCTSKRTQCGQCPMFCAAMALCTHHEILSDCPGTEAEIKQEVGKNNH 139
 Db 90 LQSVKQ--ECNRTNHNVCCEBGRY-----LEIEFLKRSRCPG3-GVQAQTPERYNY 141
 QY 140 CVPCKRGHQNTPSPARCOQPHTRCENOGIVEAPAPTAQSDTTCKNPLE 188
 Db 142 CKKCPDPGFSGETSSAPCLKHTNCSTFGILLQKGNATHDNVCNGRRE 190

RESULT 12
ID T11B HUMAN STANDARD; PRT; 401 AA.
AC 000300; 060236; Q9UHP4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
GN (osteoprotegerin) (osteoclastogenesis inhibitory factor).
OS TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA Desrose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.,
RT "osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE=lung cancer;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.,
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RP TISSUE=Placenta;
RX MEDLINE=98351569; PubMed=9688283.
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.,
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RP TISSUE=Eye;
RX MEDLINE=23888257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mitaliy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]

RP SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE=98238645; PubMed=9571159;
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.,
RT "Characterization of monomeric and homodimeric forms of
RT osteoclastogenesis inhibitory factor.";
RL Biochem. Biophys. Res. Commun. 245:382-387(1998).
RN [6]
RP SEQUENCE OF 22-393 FROM N.A.
RP TISSUE=Placenta;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.,
RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
RL Acta Biochim. Biophys. Sin. 31:680-684(1999).
RN [7]
RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX MEDLINE=97312536; PubMed=9168977;
RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA Morinaga T., Higashio K.,
RT "Isolation of a novel cytokine from human fibroblasts that
RT specifically inhibits osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 234:137-142(1997).
RN [8]
RP TRAIL BINDING.
RX MEDLINE=98269100; PubMed=9603945;
RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA Dul E., Appelbaum E.R., Eichman C., Diprinzio R., Dodds R.A.,
RA James I.E., Rosenberg M., Lee J.C., Young P.R.,
RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
RL J. Biol. Chem. 273:14363-14367(1998).
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX MEDLINE=98148058; PubMed=9478964;
RA Yamauchi K., Kinosaki M., Goto M., Kobayashi F., Tsuda E.,
RA Morinaga T., Higashio K.,
RT "Characterization of structural domains of human osteoclastogenesis
RT inhibitory factor.";
RL J. Biol. Chem. 273:5117-5123(1998).
RN [10]
RP REVIEW.
RX MEDLINE=21395914; PubMed=11505389;
RA Hofbauer L.C., Neuber A., Heutelder A.E.,
RT "Receptor activator of nuclear factor-kappaB ligand and
RT osteoprotegerin: potential implications for the pathogenesis and
RT treatment of malignant bone diseases.";
RL Cancer 92:460-470(2001).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC play a role in preventing arterial calcification. May act as decoy
CC receptor for TRAIL and protect against apoptosis. TRAIL binding
CC blocks the inhibition of osteoclastogenesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
CC lymph node, trachea, adrenal gland, testis, and bone marrow.
CC Detected at very low levels in brain, placenta and skeletal
CC muscle. Highly expressed in fetal kidney, liver and lung.
CC -!- INDUCTION: Upregulated by increasing calcium concentration in the
CC medium and estrogens. Downregulated by glucocorticoids.
CC -!- PTM: N-glycosylated. Contains static acid residues.
CC -!- SIMILARITY: The N-terminus is blocked.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 2 death domains.
CC -----
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CC EMBL; U94332; AAB53709.1; -
DR EMBL; AB002146; BAA25910.1; -
DR EMBL; AB008822; BAA32076.1; -
DR EMBL; AB008821; BAA32076.1; JOINED.
DR EMBL; BC030155; AAH30155.1; -
DR EMBL; AF134187; AAF20168.1; -
DR HSSP; P25942; ICDF.
DR Genew; HGNC:11909; TNFRSF11B.
DR MIM; 602643; -
DR GO; GO:000576; C:extracellular; TAS.
DR GO; GO:0005125; F:cytokine activity; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
KW CHAIN
FT SIGNAL 1 21
FT 22 401
FT 401 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT DOMAIN 198 269
FT DOMAIN 270 365
FT SITE 400 400
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 107 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
FT CARBOHYD 98 98
FT CARBOHYD 152 152
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
FT VARIANT 3 3
FT MUTAGEN 400 400
FT MUTAGEN 400 401
FT CONFLICT 263 263
SQ SEQUENCE 401 AA; 46040 MM; ED7448B67D86C71E CR664;

Query Match 21.1%; Score 239.5; DB 1; Length 401;
Best Local Similarity 30.9%; Pred. No. 1.7e-13;
Matches 51; Conservative 21; Mismatches 84; Indels 9; Gaps 4;

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T11B RAT
ID T11B RAT STANDARD; PRT; 401 AA.
AC 008727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin).
GN TNFRSF11B OR ORG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestine;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan U.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.,
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RT Cell 89:309-319(1997).
RL -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- INDUCTION: Upregulated by osteopontin.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -1- SIMILARITY: Contains 2 death domains.
CC -----
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CC -----
CC EMBL; U94330; AAB53707.1; -
CC HSSP; P25942; ICDF.
CC InterPro; IPR000488; Death.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 4.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS50017; DEATH DOMAIN; FALSE_NEG.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.
KW CYTOKINE; Apoptosis; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT 22 401
FT CHAIN 22 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT DOMAIN 198 269
FT DOMAIN 270 365
FT SITE 400 400
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105

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FT DISULFID 107 118 BY SIMILARITY.
FT DISULFID 124 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT DISULFID 166 185 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 401 AA; 46192 MW; FECA31F1DAE573A CRC64;

Query Match 20.8%; Score 235.5; DB 1; Length 401;
Best Local Similarity 29.6%; Pred. No. 3.7e-13;
Matches 50; Conservative 24; Mismatches 84; Indels 11; Gaps 5;

QY 23 YFEPO--HRIICSRCPGTYVASKCSRIIDVTCATCAENSYNEHMYLTICQLCRP--CDP 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 30 HYPETGRQLICDCACAPGYLKHCTVRRKTLCPDPCDYSTDSMHTSDCYVSPCKE 89
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 VMGLEELAPCTSKRKTCRCQCPGFCAMALECHGELLSDCPPTGTEALKEDEYKGNH 139
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 90 LGTVKQ--ECNRTHNRVCECEGRY-----LELEFCIKHRSCEPGL--GVLAQGTPEHNTV 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 140 CVPCKAGHPONTSSPARCOPHTRCENQGLVEAPGTAQSDTCKNPLE 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 142 CKKCPDGFPSGERTSKAPCKHTKCSLGLILKGNATHDNNVCSGNRE 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
TR14 HUMAN STANDARD; PRT; 283 AA.
ID TR14 HUMAN STANDARD; PRT; 283 AA.
AC 092956; 08WXR1; 096J31; 09UM65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor
DE (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
DE (TR2).
GN TNFRSF14 OR HVEM OR HVFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervical adenocarcinoma;
RX MEDLINE=97053782; PubMed=8898196;
RA Montgomery R.I., Warner M.S., Lam B.J., Spear P.G.;
RA "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT the TNF/NGF receptor family.";
RL Cell 87:427-436(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97306336; PubMed=9162061;
RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA Porter T.G., Tuncak A., Young P.R.;
RA "A newly identified member of the tumor necrosis factor receptor
RT superfamily with a wide tissue distribution and involvement in
RT lymphocyte activation.";
RL J. Biol. Chem. 272:14272-14276(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Cao X.;
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. AND VARIANTS ARG-17 AND ILF-241.
RX MEDLINE=21629477; PubMed=11756379;
RA Struyf F., Posavad C.M., Keyaerts E., Van Ranst M., Corey L.,
RA Spear P.G.;
RA "Search for polymorphisms in the genes for herpesvirus entry mediator,
RT Nectin-1, and Nectin-2 in immune seronegative individuals.";
RL J. Infect. Dis. 185:36-44(2002).
RN [5]

```

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RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22386257; PubMed=12477932;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Raba S.S., Loguillano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bullyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP INTERACTION WITH TRAF2 AND TRAF5.
RX MEDLINE=97298041; PubMed=9153189;
RA Heu H., Solovyev I., Colombero A., Elliott R., Kelley M., Boyle W.J.;
RT "ATAR, a novel tumor necrosis factor receptor family member, signals
RT through TRAF2 and TRAF5.";
RL J. Biol. Chem. 272:13471-13474(1997).
RN [7]
RP INTERACTION WITH TRAF3 AND TRAF5.
RX MEDLINE=97306297; PubMed=9162022;
RA Masters S.A., Ayres T.M., Skubitch M., Gray C.L., Rotte M.,
RA Ashkenazi A.;
RT "Herpesvirus entry mediator, a member of the tumor necrosis factor
RT receptor (TNFR) family, interacts with members of the TNFR-associated
RT factor family and activates the transcription factors NF-kappaB and
RT AP-1.";
RL J. Biol. Chem. 272:14029-14032(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
RX MEDLINE=21403268; PubMed=11511370;
RA Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
RA Eisenberg R.J., Wiley D.C.;
RT "Herpes simplex virus glycoprotein D bound to the human receptor
RT HveA.";
RL Mol. Cell 8:169-179(2001).
RN [9]
RP FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric
RC TNFSF14/lymphotxin-alpha. Involved in lymphocyte activation. Plays
CC an important role in HSV pathogenesis because it enhanced the
CC entry of several wildtype HSV strains of both serotypes into CHO
CC cells, and mediated HSV entry into activated human T cells.
CC - SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.
CC - TISSUE SPECIFICITY: Type I membrane protein (Probable).
CC IN LUNG, SPLEEN, AND THYMUS.
CC - SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
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DR EMBL, U70321; AAB58354.1; -
DR EMBL, U81232; AAD00505.1; -
DR EMBL, AF153978; AAF7588.1; -
DR EMBL, AF378877; AAL47717.1; -
DR EMBL, AF373878; AAL47718.1; -
DR EMBL, BC002794; AAH02794.1; -

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DR EMBL; AF068868; AAC34583.1; -;
DR EMBL; AL096801; CAB75692.1; -;
DR EMBL; BC017730; AAH17730.1; -;
DR EMBL; BC010241; AAH10241.1; ALT_INIT.
DR HSSP; 014763; 1D0G.
DR GeneW; HGNC:13469; TNFRSF21.
DR MIM; 605732; -;
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
KM Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 41 POTENTIAL.
FT CHAIN 42 655 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 42 655 SUPRAFAMILY MEMBER 21.
FT TRANSMEM 350 370 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 371 655 POTENTIAL.
FT DOMAIN 415 498 CYTOPLASMIC (POTENTIAL).
FT REPEAT 50 88 DEATH.
FT REPEAT 90 131 TNFR-CYS 1.
FT REPEAT 133 167 TNFR-CYS 2.
FT REPEAT 170 211 TNFR-CYS 3.
FT DISULFID 67 80 TNFR-CYS 4.
FT DISULFID 70 88 BY SIMILARITY.
FT DISULFID 91 106 BY SIMILARITY.
FT DISULFID 109 123 BY SIMILARITY.
FT DISULFID 113 131 BY SIMILARITY.
FT DISULFID 133 144 BY SIMILARITY.
FT DISULFID 150 168 BY SIMILARITY.
FT DISULFID 171 186 BY SIMILARITY.
FT DISULFID 192 211 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match 20.2%; Score 228.5; DB 1; Length 655;
Best Local Similarity 30.9%; Pred. No. 2.4e-12;
Matches 56; Conservative 23; Mismatches 65; Indels 37; Gaps 8;

QY 30 ICSSRCPPGTYVSAKSRIRDTVCATCAENSYNENNYLTICQLC-RPCDPVWGLEIAP 88
DB 65 ITCDDKCPAGTYVSEHCTNTSLRYVCSSPVGTFRHENGIEKCHDCSQPC-PWPMIKL-P 122
QY 89 CTSKRKTQCRQCPGMF-----CAWALECTHCEILSDCP-----PGEAEIKDEIVGK 136
DB 123 CAALTDRECTCPGWMQSNATCAPIHV-----CPVGMGVRRKGTETP----- 164
QY 137 NNHCVPCKAGHQNNTSSPARCQPHTRCENOGIVEAPGTAOSDTTCCKNPLELPPEMSG 196
DB 165 DVRCRQCAAGTFSDVPSVYMKCKAYVDCISQNLVVIKPTKETDNCVT-----LPSEFSS 220
QY 197 T 197
DB 221 T 221

Search completed: August 28, 2004, 01:49:30
Job time : 26 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 28, 2004, 01:31:38 ; Search time 115 Seconds

(without alignments)
540,496 Million cell updates/sec

Title: US-10-003-211-1

Perfect score: 1133

Sequence: 1 SQPQAVPPYASENQTCRDQF.....QSDTTCKNPLEPLPEMNSGT 197

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP rnc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriaph:*
17: SP archaep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | * Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|--------|---------------------|
| 1 | 309.5 | 27.3 | 483 | 13 | Q800K7 | Q800K7 paracanth |
| 2 | 295.5 | 26.1 | 278 | 6 | Q8SQ34 | Q8SQ34 sus scrofa |
| 3 | 291.5 | 25.7 | 433 | 11 | Q91ZM6 | Q91ZM6 rattus norv |
| 4 | 291.5 | 25.7 | 474 | 11 | Q80WY6 | Q80WY6 rattus norv |
| 5 | 290 | 25.6 | 459 | 11 | Q62327 | Q62327 mus musculu |
| 6 | 284.5 | 25.1 | 274 | 6 | Q7YRL5 | Q7YRL5 canis fami |
| 7 | 278 | 24.5 | 223 | 4 | Q86YK5 | Q86YK5 homo sapien |
| 8 | 276.5 | 24.4 | 482 | 11 | Q88734 | Q88734 mus musculu |
| 9 | 265.5 | 23.4 | 277 | 6 | Q8WMO2 | Q8WMO2 ovis aries |
| 10 | 258 | 22.8 | 275 | 11 | Q80WM9 | Q80WM9 mus musculu |
| 11 | 253 | 22.3 | 462 | 13 | Q805B0 | Q805B0 gallus galli |
| 12 | 243.5 | 21.5 | 289 | 11 | Q8KX26 | Q8KX26 mus musculu |
| 13 | 242.5 | 21.4 | 283 | 6 | Q9X528 | Q9X528 cercopithec |
| 14 | 240 | 21.2 | 186 | 12 | Q72735 | Q72735 compox viru |
| 15 | 238.5 | 21.1 | 318 | 13 | Q7T2H3 | Q7T2H3 oncorhynch |
| 16 | 238 | 21.0 | 302 | 13 | Q9PU50 | Q9PU50 salvelinus |

| | | | | | | |
|----|-------|------|-----|----|--------|---------------------|
| 17 | 233.5 | 20.6 | 457 | 4 | Q8IVS6 | Q8IVS6 homo sapien |
| 18 | 232.5 | 20.5 | 467 | 13 | Q800I0 | Q800I0 gallus galli |
| 19 | 230 | 20.3 | 276 | 13 | Q9DD2 | Q9DD2 gallus galli |
| 20 | 230 | 20.3 | 351 | 12 | Q57117 | Q57117 compox viru |
| 21 | 229.5 | 20.3 | 285 | 13 | Q90W71 | Q90W71 oncorhynch |
| 22 | 228.5 | 20.0 | 167 | 12 | Q8UYL3 | Q8UYL3 vaccinia vi |
| 23 | 225.5 | 19.9 | 186 | 13 | Q722Y5 | Q722Y5 gallus galli |
| 24 | 225.5 | 19.9 | 651 | 13 | Q98SM6 | Q98SM6 gallus galli |
| 25 | 225 | 19.9 | 186 | 12 | Q9YP87 | Q9YP87 compox viru |
| 26 | 225 | 19.9 | 349 | 12 | Q57099 | Q57099 monkeypox v |
| 27 | 225 | 19.9 | 349 | 12 | Q57098 | Q57098 monkeypox v |
| 28 | 225 | 19.9 | 349 | 12 | Q57284 | Q57284 camelipox vi |
| 29 | 223 | 19.7 | 186 | 12 | Q91LR5 | Q91LR5 vaccinia vi |
| 30 | 221.5 | 19.5 | 285 | 13 | Q90XS6 | Q90XS6 oncorhynch |
| 31 | 221 | 19.5 | 349 | 12 | Q57100 | Q57100 monkeypox v |
| 32 | 220.5 | 19.5 | 349 | 12 | Q57097 | Q57097 monkeypox v |
| 33 | 220 | 19.5 | 169 | 11 | Q9UXE0 | Q9UXE0 rattus norv |
| 34 | 219 | 19.3 | 349 | 12 | Q57102 | Q57102 monkeypox v |
| 35 | 219 | 19.3 | 349 | 12 | Q57291 | Q57291 monkeypox v |
| 36 | 218.5 | 19.3 | 167 | 12 | Q9DUJ2 | Q9DUJ2 compox viru |
| 37 | 218.5 | 19.3 | 350 | 12 | Q57116 | Q57116 compox viru |
| 38 | 218 | 19.2 | 186 | 12 | Q9WJB4 | Q9WJB4 vaccinia vi |
| 39 | 218 | 19.2 | 348 | 12 | Q57108 | Q57108 monkeypox v |
| 40 | 218 | 19.2 | 267 | 6 | Q02764 | Q02764 oryctolagus |
| 41 | 217.5 | 19.2 | 348 | 12 | Q57103 | Q57103 monkeypox v |
| 42 | 216.5 | 19.1 | 167 | 12 | Q57272 | Q57272 compox viru |
| 43 | 216 | 19.1 | 348 | 12 | Q57277 | Q57277 monkeypox v |
| 44 | 216 | 19.1 | 349 | 12 | Q57101 | Q57101 monkeypox v |
| 45 | 210 | 18.5 | 348 | 12 | Q57112 | Q57112 variola vir |

ALIGNMENTS

RESULT 1

| ID | Q800K7 | PRELIMINARY; | PRT; | 483 AA. |
|----|--|--------------|------|---------|
| AC | Q800K7; | | | |
| DT | 01-JUN-2003 (TREMURel. 24, Created) | | | |
| DT | 01-JUN-2003 (TREMURel. 24, Last sequence update) | | | |
| DT | 01-OCT-2003 (TREMURel. 25, Last annotation update) | | | |
| DE | Tumor necrosis factor receptor-2. | | | |
| GN | TNFR-2. | | | |
| OS | Paralichthys olivaceus (Flounder). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; | | | |
| OC | Acanthomorpha; Acanthopterygii; Perciforma; Pleuronectiformes; | | | |
| OC | Pleuronectoidei; Paralichthyidae; Paralichthys. | | | |
| OX | NCBI_TaxID=8255; | | | |
| FN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Park C., Kurobe T., Hirano I., Aoki T.; | | | |
| RT | "Cloning and characterization of cDNAs for two distinct tumor necrosis | | | |
| RT | factor receptor superfamily genes from Japanese flounder Paralichthys | | | |
| RT | olivaceus." | | | |
| RL | Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AB080947; BAC6526.1; - | | | |
| DR | GO; GO:0004872; F-receptor activity; IEA. | | | |
| DR | InterPro; IPR001368; TNFR_c6. | | | |
| DR | SMART; SM00208; TNFR_c6; 3. | | | |
| DR | SMART; SM00208; TNFR_c6; 4. | | | |
| DR | PROSITE; PS00652; TNFR_NGFR_1; 1. | | | |
| DR | PROSITE; PS00650; TNFR_NGFR_2; 3. | | | |
| KW | Receptor | | | |
| SQ | SEQUENCE 483 AA; 52227 MW; EE55874A8C7F2085 CRC64; | | | |

Query Match 27.3%; Score 309.5; DB 13; Length 483;

Best Local Similarity 35.4%; Pred. No. 2.9e-25;

Matches 64; Conservative 20; Mismatches 80; Indels 17; Gaps 6;

QY 16 CRDQEKYEPQRIKCSRCPTGYTSACSRIRDTVCATCAENSYNEHNNYLTICQLCR 75
DB 27 CHNSTEYRQD--LCKKCPGQRIKQCSDATEBSVCQCSGQYMEKWNVAKQCLSCN 84

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QY 76 PCDPVWGLBEIAPCTSKRKTQCRCPQMFCAWALB-----CTHCELLSDCPPTGAELK 130
DB 85 KCKSKNGLOYAORCSSITTRIGCYCKRGMYC---IMFDNPNYACBANCYSCRAGYGVSLP 141
QY 131 DEVGKNN--HCVPCKAGHFONTSSPARCOPHTRCENOGUVEAAGTAOSDTTCNNPLE 188
DB 142 ---GKANSVCKELCPDGMFSNTSSMTETCRPHTDGKAVVR--KANTTSDTVCEBGVA 196
QY 189 P 189
DB 197 P 197

RESULT 2
Q88Q34 PRELIMINARY; PRT; 278 AA.
ID Q88Q34;
AC Q88Q34;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE CD40.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA West K.A., Li A.W., Rowden G.;
RT "Characterization of the Porcine CD40 Molecule.";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF248545; AAL92924.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR01368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
SQ SEQUENCE 278 AA; 30951 MW; 20D46B44AF93DD2 CRC64;

Query Match 26.1%; Score 295.5; DB 6; Length 278;
Best Local Similarity 36.9%; Pred. No. 5.4e-24;
Matches 62; Conservative 19; Mismatches 74; Indels 13; Gaps 3;

QY 21 KEYEPOHRIICSRCPPTGYVSAKCSRIRDTVCATCAENSYNEHNNYLTTCQLCRPCDPV 80
DB 27 KENQPTNRSRCNLCPGQKLVNHCETVETELCLPCSSSEFLATNRRKHCQHKYCDPN 86
QY 81 MGLIEIAPCTSKRKTQCRCPQMFCAWALBECTHCELLSDCPG-----TEALDVEVK 135
DB 87 IGLQVREGTSKTDITVCSEGHCTNSA--CESCTHSLCPFGGVKOMATEVSDTI-- 142
QY 136 GNNHCVPCKAGHFONTSSPARCOPHTRCENOGUVEAAGTAOSDTTC 183
DB 143 ---GKCPVGFPSNVSSASEKQCPMTSCSKGLVQKAGTKTIDVVC 186

RESULT 3
Q91ZM6 PRELIMINARY; PRT; 433 AA.
ID Q91ZM6;
AC Q91ZM6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tumor necrosis factor receptor type II (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley;
RA Oebury B., Pelser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT capillary endothelial cells and participate in TNF-alpha transport
RT through the blood-brain barrier.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF420214; AAL16021.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1
FT TER 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

Query Match 25.7%; Score 291.5; DB 11; Length 433;
Best Local Similarity 33.3%; Pred. No. 2.3e-23;
Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

QY 8 PYASENCTCDQEKYEYEPQHRICSRCPPTGYVSAKCSRIRDTVCATCAENSYNEHNNY 67
DB 11 PYKEPNNCCQISOETYDKAQMCAKCPQGVAKHCNKTSDVVCADCAAGMFTQVWNH 70
QY 68 LITICOLC-RPC--DPVWGLBEIAPCTSKRKTQCRCPQMFCA--AMALECTHCELLSDCP 122
DB 71 LHTGLCSSSSCSDDQV---ETHNCTKKQNVCACMNDSYCALKLHSGNCRCQMKLSKCG 126
QY 123 PGTAEFLKDEYKGNKNCVPCKAGHFONTSSPARCOPHTRCENOGUVEAAGTAOSDTT 182
DB 127 PGF-GVARSRTSNVNICACAPGTFSDTISTVCRPHRICS---ILALPGNASTDAY 181
QY 183 CKNLEPLPEMSEGT 197
DB 182 CASE-SPTPSAVPRT 195

RESULT 4
Q80WY6 PRELIMINARY; PRT; 474 AA.
ID Q80WY6;
AC Q80WY6;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor type II.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Mistar; TISSUE=Spleen;
RA Li Y., Li A., Schafer M.K.;
RT "Expression of TNFR2 in rat dorsal root ganglion.";
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF498039; AAP3151.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 474 AA; 50148 MW; 298C6AB9E8C8D714 CRC64;

Query Match 25.7%; Score 291.5; DB 11; Length 474;
Best Local Similarity 33.3%; Pred. No. 2.6e-23;

```

Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

QY 8 PYASNOTCRDQEKYEYEPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNEHNYL 67
Db 31 PYKPEPGNQCIQSQ-EYDRAKQCMCAKCPGQYVKKHCKNTSDTVCADCSAWTYQVWN 74
QY 68 LTICQLC-RPC--DPMGLEIAPCTSKRTQCRQCPGMFCA--AMALECTHCELLSDCP 122
Db 91 LHTCLSSSSCSDDV---ETHNCTKKQNRVCAENADSYCALKLHSGNCRQCMKLSKCG 146
QY 123 PGTEAEIKDEVGKNNHCVPCKAGHFONTSSPSARCOPHTRCENOGIVEAAPTASDPT 182
Db 147 PGF-GVASSRKTSGNVICSAAPGTFTSDTTSIDVCRPHRIS---TLAIPGASTDAV 201
QY 183 CKNPLEPLPPEMSGT 197
Db 202 CASE-SPTPSAVPRT 215

RESULT 5

Q62327 PRELIMINARY; PRT; 459 AA.
AC Q62327;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE Murine tumour necrosis factor receptor 2 protein (Fragment).
GN TNFRSF1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RC "Amino acid variation in the tumor Necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice.";
RL Genomics 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=85178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5:726-727 (1994).
DR EMBL: X76401; CAAS3981.1; -.
DR PIR: I48854; I48854.
DR HSSP: P19438; INCF.
DR MCD; MG1:1314883; TNFRsf1b.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0008320; P:necrosis; IMP.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KM Receptor.
FT NON TER 1
FT VARIANT 87 1
FT VARIANT 87 S -> T.
FT VARIANT 93 T -> I.
FT VARIANT 268 F -> I.
FT VARIANT 345 S -> F.
FT VARIANT 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 25.6%; Score 290; DB 11; Length 459;
Best Local Similarity 33.5%; Pred. No. 3.6e-23;
Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;

QY 8 PYASE-NQTCRDEKYEYEPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNEHNYL 66

Db 16 PYKPEPGYEQISQ-EYDRAKQCMCAKCPGQYVKKHCKNTSDTVCADCSAWTYQVWN 74
QY 67 YLTICQLC---PDDPMGLEIAPCTSKRTQCRQCPGMFCA--AMALECTHCELLSDC 121
Db 75 QFRTCLSSSSCSSTDV---ETRACTKQNRVCAENADSYCALKLHSGNCRQCMKLSKCG 130
QY 122 PGTEAEIKDEVGKNNHCVPCKAGHFONTSSPSARCOPHTRCENOGIVEAAPTASDPT 181
Db 131 PGF-GVASSRKTSGNVICSAAPGTFTSDTTSIDVCRPHRIS---TLAIPGASTDA 185
QY 182 TCNPLEPLPPEMSGT 195
Db 186 VC---APESPTLS 195

RESULT 6

Q7YRL5 PRELIMINARY; PRT; 274 AA.
AC Q7YRL5;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE CD40.
GN CD40.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang S., Sim G.-K.;
RT "Canine CD40 and CD40 ligand cDNA Sequences.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY333789; AAB6653.1; -.
SQ SEQUENCE 274 AA; 30284 MW; 9723789A07BAB6DB CRC64;

Query Match 25.1%; Score 284.5; DB 6; Length 274;
Best Local Similarity 34.9%; Pred. No. 8.4e-23;
Matches 61; Conservative 18; Mismatches 89; Indels 7; Gaps 4;

QY 9 YASENOTCRDQEKYEYEPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNEHNYL 68
Db 19 YPEPRYACR--EKQYLVDSQ--CCNMCPEKXVNDCLHTIDECTRCQGFIDTWNAE 74
QY 69 TICQLCRCPDPMGLEIAPCTSKRTQCRQCPGMFCAAMALCTHCELLSDCPGTEAB 128
Db 75 RHCHQHKKYCDPNLGLHVEKKGTSBTDTCDCDGLHCTNAA--CESCTWHLCPPGIGVK 132
QY 129 LKDEVGKNNHCVPCKAGHFONTSSPSARCOPHTRCENOGIVEAAPTASDPTTC 183
Db 133 -QIATGISDITCPCPIGPFSSNVSALEKCHPWTSCETKGLVQAGTNTKTDVYC 186

RESULT 7

Q86YK5 PRELIMINARY; PRT; 223 AA.
AC Q86YK5;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 (Fragment).
GN TNFRSF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA He X., Xu L., Zeng Y.;
RT "Transcripts of CD40 isoform in peripheral mononuclear cells.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY225405; AAO43990.1; -.

DR GO:0016020; C:membrane; IEA.
DR GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO:0005488; F:binding; IEA.
DR GO:0004888; F:transmembrane receptor activity; IEA.
DR GO:0006915; F:apoptosis; IEA.
DR GO:0006955; P:immune response; IEA.
DR GO:0007165; P:signal transduction; IEA.
DR GO:0006810; P:transport; IEA.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR008063; Fas_receptor.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00202; TNFR_c6; 4.
DR PRINTS: PR01680; FASRECEPTOR.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00215; MITOCH_CARRIER; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 4.
KM Receptor.
FT NON TER 223
SQ SEQUENCE 223 AA; 24659 MW; 85C63C20BC4E0B1C CRC64;

Query Match 24.5%; Score 278; DB 4; Length 223;
Best Local Similarity 35.0%; Pred. No. 3.5e-22;
Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;
QY 7 PPSVSENOTCRDDEKEYEPQHRICSRCPGTYSAKSRIRDTVCATCAENSYNEHWN 66
DB 22 PPTA-----CR--EKQYIINSQ--CCSICGQCGQVSDVSCFTFTTECLPCESSFLDTWN 72
QY 67 YLTICQCRPCDPYWGIEIAPCTSKRKTQCRQPGMCAAMALECTHCELLSDCPETE 126
DB 73 RETHGHQKXCDPMLGLRQVQKSETPTICTCEBGMHCTSEA--CESCVLHRSQSPFG 130
QY 127 AELKDEVGKNNHCVPCKAGHPONTSSSARCOPIHRENGVLEAANGTQSDPTC 183
DB 131 VK-QIATGVSPTLICEPCVGFPSNVSSAFKCHPWTSCETRDVLVQAGTKKTDVVC 186

RESULT 8
ID 088734 PRELIMINARY; PRT; 482 AA.
AC 088734;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE P80 TNF-alpha receptor.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98414512; PubMed=9740674;
RA Hurlb F., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
and Characterization of the two Transcripts.";
RL Genomics 52:79-98(1998).
DR EMBL: Y14619; CAA74969.1; JOINED.
DR EMBL: Y14620; CAA74969.1; JOINED.
DR EMBL: Y14621; CAA74969.1; JOINED.
DR EMBL: Y14622; CAA74969.1; JOINED.
DR EMBL: Y14623; CAA74969.1; JOINED.
DR EMBL: Y14679; CAA74969.1; JOINED.
DR HSSP: Q92956; IJMA.
DR GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00202; TNFR_c6; 4.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.

KM Receptor.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FE93C CRC64;
Query Match 24.4%; Score 276.5; DB 11; Length 482;
Best Local Similarity 32.3%; Pred. No. 1.1e-21;
Matches 65; Conservative 24; Mismatches 85; Indels 27; Gaps 9;
QY 8 PPSVSENOTCRDDEKEYEPQHRICSRCPGTYSAKSRIR-----RDTVCATCAEN 59
DB 31 PYKPEFGYECQISQ-EYDRKAMCCAKCPGQGVNHFCKMTSDTVCADSDTVACADCEAS 89
QY 60 SYNEHNNVLTICQLCE--PCDPWGLIEIAPCTSKRKTQCRQPGMCA--AMALECTH 114
DB 90 MYQVWNNQRFITLCSSCSTQDV---ETRACTKQONRVCAQCBAGRYCALKTHSGSCRO 145
QY 115 CELLSDCPTEHELDVCKGNNHCVPCKAGHPONTSSSARCOPIHRENGVLEAANGTQSDPTC 174
DB 146 CMRLSKCGPGF-GVASSRAPNGVLCACAPGTFPSDTTSTSDVCRPHRIS-----ILAI 200
QY 175 GTAQSDPTCKNPLEPPEMS 195
DB 201 GNASTDVAVC---APESPITLS 217

RESULT 9
ID 088M02 PRELIMINARY; PRT; 277 AA.
AC 088M02;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Membrane protein CD40 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Zawitkowski M.S., Russ G.R., Krishnan R.;
RT "Cloning and expression of the ovine CD40 molecule and the inhibition
of the mixed lymphocyte reaction by the ovine CD40-EGFP fusion
protein.";
RT protein.
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY072798; AAL68402.1; -.
DR GO:0016020; C:membrane; IEA.
DR GO:0004888; F:transmembrane receptor activity; IEA.
DR GO:0006915; F:apoptosis; IEA.
DR GO:0006955; P:immune response; IEA.
DR GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR008063; Fas_receptor.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00202; TNFR_c6; 4.
DR PRINTS: PR01680; FASRECEPTOR.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
FT NON TER 277
SQ SEQUENCE 277 AA; 30465 MW; 619F28BEA18A0D29 CRC64;

Query Match 23.4%; Score 265.5; DB 6; Length 277;
Best Local Similarity 33.7%; Pred. No. 1e-20;
Matches 56; Conservative 21; Mismatches 80; Indels 9; Gaps 4;
QY 20 EKEYEPQHRICSRCPGTYSAKSRIRDTVCATCAENSYNEHNNVLTICQLCRPCDP 79
DB 28 EKQY--PVNSLCCDULCPQCKLINDCTRYSKTRBCQSCGGEFLSTNREKYCHEHRYCNP 85
QY 80 VMLIEIAPCTSKRKTQCRQPGMCAAMALECTHCELLSDCPGTBAELKDEVGK--N 137
DB 86 NLGLRQSGTINTDTTVCDEGQHTSHT--CESCTPHSLCLPGRGVK--QIATGVLD 140
QY 138 NHCVPCKAGHPONTSSSARCOPIHRENGVLEAANGTQSDPTC 183


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Db      141 TICEPCVGFPSNVSAFEKCHPWTSCERKGLVQHVGWTKNTDVC 186
RESULT 10
Q80WM9 PRELIMINARY; PRT; 275 AA.
AC Q80WM9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Thymus;
RA Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.,
RT "Light regulation in a murine model of ovarian carcinoma."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY264405; AAC09081.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR008063; Fas receptor.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KM Receptor; Signal.
FT SIGNAL 1 38 Potential.
SQ SEQUENCE 275 AA; 30171 MW; C4ATVADBEFC0521D CRC64;

Query Match 22.8%; Score 258; DB 11; Length 275;
Best Local Similarity 34.8%; Pred. No. 6,6e-20;
Matches 63; Conservative 14; Mismatches 86; Indels 18; Gaps 6;

QY 11 SENQTCRDOKEYEYEPQRIICSRCPGTYVSACSRIRDTVCATCAENSYNEMNYLT 70
Db 37 SAQPSCKQEBEFLVDE----CPMCNPGYHVKQVCSBHTGTVCAPCPQYTYAHANGLSK 92
QY 71 CQICRCPDPMGLIEIAPCTSKRTQCRQCPGFCAM ALECHGELSDCPTGTAEL 129
Db 93 CLPCGVCDPMGLITWQECSSMKDTVCRIPGYFCENQDSHCSSTCIQHTTCEPQGRVE- 151
QY 130 KDEVGKGNH-----CVPCKAGHFONTSSPARCQPHTRCENQGLVEAAPGTASDPTTK 184
Db 152 -----KRGTHDQDTVCADCLTGTFF-SLGTQEBECLPWTNC-SAFQGEVRRGNTSTDTTCS 204
QY 185 N 185
Db 205 S 205

RESULT 11
Q805B0 PRELIMINARY; PRT; 462 AA.
AC Q805B0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor receptor-II.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

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OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn H-B15; TISSUE=Spleen;
RA Sayde A.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn H-B15; TISSUE=Spleen;
RA Sayde A.A., Horuchi H., Furusawa S., Matsuda H.;
RT "Molecular cloning and characterization of chicken tumor necrosis
RT factor receptor-II (TNFR-II) and tumor necrosis factor receptor
RT associated factor-5 (TRAF-5) genes."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB101004; BAC5966.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR008063; Fas receptor.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KM Receptor.
SQ SEQUENCE 462 AA; 50141 MW; 8B00A93305414782 CRC64;

Query Match 22.3%; Score 253; DB 13; Length 462;
Best Local Similarity 29.4%; Pred. No. 3.9e-19;
Matches 59; Conservative 24; Mismatches 100; Indels 18; Gaps 6;

QY 8 PYASNQTCRDOKEYEYEPQRIICSRCPGTYVSACSRIRDTVCATCAENSYNEMNY 67
Db 23 PYTPQSAQCNPSFTEFEELKRCCKSCPGRKABSCSHSVTKICPLCPDTYAVWNR 82
QY 68 LITICQLCR-PCDPMGLIEIAPCTSKRTQCRQCPGFCAMALE-CTHCEGLSDCPTGT 125
Db 83 SPQCFAPSPCCR-KGFVENQTTILSMDRICSPPNRYCISKYQNKCHICKVAKKCGRY 140
QY 126 EAEIKDEVGKGNHCVPCAKAGHFONTSSPARCQPHTRCENQGLVEAAPGTASDPTTKN 185
Db 141 RVSRRG-TDSTDECKPCPGTFSDSDSYTSCIPHIVCKS---VAVAGNNVNDITVCHD 195
QY 186 PLRP-----LPPEMSGT 197
Db 196 SVATALPHTRAVNPLPQSSST 216

RESULT 12
Q8KXK6 PRELIMINARY; PRT; 289 AA.
AC Q8KXK6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC029254; AAH29254.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0005840; C:ribosome; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.

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| ID | Q9XSZ8 | PRELIMINARY | PRT | 283 AA. |
|----|--|---|----------------|------------------------|
| DR | GO: 0004888; F:transmembrane receptor activity; IEA. | | | |
| DR | GO: 0006915; P:apoptosis; IEA. | | | |
| DR | GO: 0006915; P:immune response; IEA. | | | |
| DR | GO: 0006412; P:protein biosynthesis; IEA. | | | |
| DR | GO: 0007165; P:signal transduction; IEA. | | | |
| DR | InterPro: IPR008063; Fas receptor. | | | |
| DR | InterPro: IPR001005; Myb DNA binding. | | | |
| DR | InterPro: IPR001865; Ribosomal_S2. | | | |
| DR | InterPro: IPR001368; TNFR_C6. | | | |
| DR | Pfam: PF00020; TNFR_C6; 4. | | | |
| DR | PRINTS: PR01680; FASRECEPTOR. | | | |
| DR | SMART: SMO0208; TNFR; 4. | | | |
| DR | PROSITE: PS00037; MYB_1; 1. | | | |
| DR | PROSITE: PS00862; RIBOSOMAL_S2_1; 1. | | | |
| DR | PROSITE: PS00652; TNFR_NGFR_1; 1. | | | |
| DR | PROSITE: PS00505; TNFR_NGFR_2; 4. | | | |
| DR | Receptor. | | | |
| DR | SEQUENCE | 289 AA; | 32077 MW; | DB93B1E439F1E2A CRC64; |
| DR | Query Match | 21.5%; | Score 243.5; | DB 11; Length 289; |
| DR | Best Local Similarity | 31.0%; | Pred. 2.6e-18; | |
| DR | Matches | 54; Conservative | 22; Mismatches | 81; Indels 17; Gaps 5 |
| DR | 15 | TCRDENEKYEYEPQHRICCSRCPPGTYSAAKSRIRDYCATCAENSYNENHNYLTICQLC | 74 | |
| DR | 25 | TCSD--KQYLHDGQ--CCDLCPGSRRLSHCTALAKTQCHPCDSGSEFSAQNRRLRCHQH | 80 | |
| DR | 75 | RPCDPVMGLIEBIAFPTCKSRKRTQCRQCPGFCAMALICTHGLSDCPRG---TEAFL | 129 | |
| DR | 81 | RHCEPNQGLRVAKKEGTAEISDTVCACKEGHCT--SKDCACAKQHTPCIPGFGWMEMATET | 138 | |
| DR | 130 | KDEVGKANNHCYPCAKAGHQNNTSSSARCPQPHTRCENQSLVAAAGTAQSDTTC | 183 | |
| DR | 139 | TDTV-----CHPCPYGFFSNQSSLEFKCYPWTISGDKNLVLYQKSTQTNVIC | 186 | |
| DR | RESULT 13 | | | |
| DR | Q9XSZ8 | PRELIMINARY | PRT | 283 AA. |
| DR | AC | Q9XSZ8; | | |
| DR | DT | 01-NOV-1999 (TREMBLrel. 12, Created) | | |
| DR | DT | 01-NOV-1999 (TREMBLrel. 12, Last sequence update) | | |
| DR | DT | 01-JUN-2003 (TREMBlrel. 24, Last annotation update) | | |
| DR | DE | Hveas. | | |
| DR | GN | Hveas. | | |
| DR | OS | Cercopithecus aethiops (Green monkey) (Grivet). | | |
| DR | OC | Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| DR | OC | Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; | | |
| DR | OC | Cercopitheciinae; Cercopithecus. | | |
| DR | OK | NCBI_TaxId=9534; | | |
| DR | RN | [1] | | |
| DR | RP | SEQUENCE FROM N.A. | | |
| DR | RC | TISSUE=Kidney; | | |
| DR | RX | MEDLINE=99296730; PubMed=10366573; | | |
| DR | RA | Foster T.P., Chouljenko V.N., Kousoulas K.G.; | | |
| DR | RT | "Functional characterization of the Hvea homolog specified by African | | |
| DR | RT | green monkey kidney cells with a herpes simplex virus expressing the | | |
| DR | RT | green fluorescence protein."; | | |
| DR | RL | Virology 258:365-374 (1999). | | |
| DR | DR | EMBL: AF147720; AAD37381.1; -- | | |
| DR | DR | HSSP: Q92956; LUMA. | | |
| DR | DR | GO: 0016020; C:membrane; IEA. | | |
| DR | DR | GO: 0004888; F:transmembrane receptor activity; IEA. | | |
| DR | DR | GO: 0006915; P:apoptosis; IEA. | | |
| DR | DR | GO: 0006915; P:immune response; IEA. | | |
| DR | DR | GO: 0007165; P:signal transduction; IEA. | | |
| DR | DR | InterPro: IPR008063; Fas receptor. | | |
| DR | DR | InterPro: IPR001368; TNFR_C6. | | |
| DR | DR | Pfam: PF00020; TNFR_C6; 3. | | |
| DR | DR | PRINTS: PR01680; FASRECEPTOR. | | |
| DR | DR | SMART: SMO0208; TNFR; 3. | | |
| DR | DR | PROSITE: PS00652; TNFR_NGFR_1; 1. | | |
| DR | DR | PROSITE: PS00505; TNFR_NGFR_2; 2. | | |

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|-----------|---|--|--------------------|------------------|--------------------|
| SO | SEQUENCE | 283 AA; | 3019 MW; | 397951C6617EE3AA | CRC64; |
| | Query Match | 21.4%; | Score 242.5; | DB 6; | Length 283; |
| | Best Local Similarity | 32.2%; | Pred. No. 3.3e-16; | | |
| | Matches | 57; | Conservative 18; | Mismatches 85; | Indels 17; Gaps 6; |
| OY | 9 | YASNNQTCRDEKRYEPEQHRIICSRCPPTGYVSAKSRIIDPYCATCAENSYNEHMYNL 68 | | | |
| | : | : : | : | : | : |
| Db | 35 | YAPALPSC--EDLEY--PVSECCPKGPGPHVQAAGEQGTGCVCPSPTYIAHPNGL 90 | | | |
| OY | 69 | TICQLCRPCDPVMGLEIAPCTSKRKTCRCQPFGFCAM-ALEETHELLSDCPRTGA 127 | | | |
| | : | : : | : | : | : |
| Db | 91 | SKLCIQCCDCDPAWGILFTSRNCSTJANMLCGSPGHFCLIIODGDHCACARAVATSSPG--- 147 | | | |
| OY | 128 | ELKBEVGKGNH-----CVPKAGHPONTSSPSARCOPHTCENCGLVEAAPGTQS 179 | | | |
| | : | : | : | : | : |
| Db | 148 | --ORVOKGTESQDTLCONCPPGF--SSNGTLBECQHGKCSKMVLVBAGRTSSS 200 | | | |
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| RESULT 14 | | | | | |
| ID | 072735 | PRELIMINARY; | PRT; | 186 AA. | |
| AC | 072735; | | | | |
| DT | 01-AUG-1998 (TREMBLrel. 07, Created) | | | | |
| DT | 01-AUG-1998 (TREMBLrel. 07, Last sequence update) | | | | |
| DD | 01-JUN-2003 (TRMBLrel. 24, Last annotation update) | | | | |
| DE | A56k protein. | | | | |
| GN | A56K. | | | | |
| OS | Cowpox virus (CPV). | | | | |
| OC | Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; | | | | |
| OC | Orthopoxvirus. | | | | |
| OX | NCB1_TaxID=10243; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=GRI-90; | | | | |
| RX | MEDLINE=97068532; PubMed=9568042; | | | | |
| RA | Safonov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V., Petrov N.A., Shchelkunov S.N., Sandakchiev L.S.; | | | | |
| RT | "Genes of a circle of hosts for the cowpox virus."; | | | | |
| RL | Dokl. Akad. Nauk 349:829-833(1996). | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=GRI-90; | | | | |
| RA | Shchelkunov S.N., Safonov P.F., Totmenin A.V., Miheev M.V., Ryzanankina O.I., Petrov N.A., Gutarov V.V., Kotwal G.J.; | | | | |
| RT | "Structure-function and organization of cowpox virus strain GRI-90 complete genome."; | | | | |
| RL | Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases. | | | | |
| RN | [4] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=GRI-90; | | | | |
| RA | Totmenin A.V.; | | | | |
| RL | Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases. | | | | |
| EMBL | X94355; CAD90723.1; -- | | | | |
| HSSP | Q92956; IUMA | | | | |
| GO | GO:0004872; F:receptor activity; IEA. | | | | |
| InterPro | IPR001366; TNFR_c6. | | | | |
| Pfam | PF00020; TNFR_c6; 2. | | | | |
| SMART | SM00208; TNFR_2. | | | | |
| PROSITE | PS00652; TNFR_NGPR_1; 2. | | | | |
| PROSITE | PS50050; TNFR_NGPR_2; 2. | | | | |
| SEQUENCE | 186 AA; 20482 MW; D2342F1040AD0AE3 CRC64; | | | | |

Query Match 21.2%; Score 240; DB 12; Length 186;
 Best Local Similarity 32.2%; Pred. No. 4e-18;
 Matches 48; Conservative 25; Mismatches 66; Indels 10; Gaps 5;

QY 3 POAVPPASNNQCRDQEKRYEPORICSRCPPTGYVSAAKSRIRDTYCATCAENSYN 62
 DB 24 PTLPPAPVNGSC--DEGEYLDKRNQCNCQCPGFAVRCSGSDNTYCERCPPHTYT 81
 QY 63 EHNWYLLTICQLCRPCDPVWGLEBRIAPCTSKRTQCRCQPMFCA--AMALECTHCELLS 119
 DB 82 AIPNYSNGCHQCKRC-PTGSFDPKY-KCTGTQNSKSCSLPQMYCATDSQTEDCRDVCVPS 139
 QY 120 DCPPTGEALDKDEVGKNNHCVPCKAGHF 148
 DB 140 RCPGCGYFGIDQ--GNPICKSCVGEY 165

RESULT 15

Q7T2H3 PRELIMINARY; PRT; 318 AA.
 ID Q7T2H3
 AC Q7T2H3;
 DT 01-OCT-2003 (TREMblrel. 25, Created)
 DT 01-OCT-2003 (TREMblrel. 25, last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
 DE Tumour necrosis factor receptor.
 GN TNFR.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head kidney;
 RA Zou J., Secombes C.J.;
 RT "Molecular cloning and expression analysis of a TNF receptor homologue
 in rainbow trout, Oncorhynchus mykiss.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ517804; CAD57165.1; -;
 KM Receptor.
 SQ SEQUENCE 318 AA; 35254 MW; 78F8135011283B43 CRC64;

Query Match 21.1%; Score 238.5; DB 13; Length 318;
 Best Local Similarity 29.1%; Pred. No. 1e-17;
 Matches 50; Conservative 22; Mismatches 89; Indels 11; Gaps 3;

QY 16 CRDQEKRYEPORICSRCPPTGYVSAAKSRIRDTYCATCAENSYNEHNNYLLTICQLCR 75
 DB 6 CKTEEYLDASGVKRCRCRKGQYRTDCKSTKTECTCQHEYYTAELNFKQCLPCR 65
 QY 76 PCDPVWGLEBRIAPCTSKRTQCRCQPMFCAAMALECTHCELLSDCPPTGEALDKDEVK 135
 DB 66 VCYSNNQKYLRECEASDRQCYCKTGYICTDDG--CEHCLPYTLCPGSSGV-----VNG 118
 QY 136 GNNH---CVPCKAGHFQNTSSPSARCQPHTRCENQGLVBAAPGTAQSDTTC 183
 DB 119 ANPQNDTVCAPQCPGTYSFNDAFTHCQSTRCGDLGKVKVSAAGTETTDVAVC 170

Search completed: August 28, 2004, 01:49:03
 Job time : 119 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 01:44:58 ; Search time 32 Seconds

(without alignments)
317.822 Million cell updates/sec

Title: US-10-003-211-1
Perfect score: 1133
Sequence: 1 SQPQAVPPYASNCQCDQE.....QSDTCKNPLEPPENSGT 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 1133 | 100.0 | 197 | 4 | US-09-000-166-1 |
| 3 | 1133 | 100.0 | 197 | 4 | US-09-303-262-1 |
| 4 | 987 | 87.1 | 170 | 4 | US-08-828-683A-14 |
| 5 | 981 | 86.6 | 170 | 4 | US-09-523-323-57 |
| 6 | 771 | 68.0 | 415 | 3 | US-09-006-353A-6 |
| 7 | 771 | 68.0 | 415 | 4 | US-09-573-986-6 |
| 8 | 456 | 40.2 | 77 | 3 | US-08-866-545-3 |
| 9 | 456 | 40.2 | 77 | 4 | US-09-627-775-3 |
| 10 | 305 | 26.9 | 227 | 3 | US-08-974-022-48 |
| 11 | 305 | 26.9 | 227 | 3 | US-08-795-445A-48 |
| 12 | 305 | 26.9 | 227 | 3 | US-08-795-447A-48 |
| 13 | 305 | 26.9 | 227 | 3 | US-08-974-186-48 |
| 14 | 305 | 26.9 | 227 | 3 | US-08-795-446A-48 |
| 15 | 305 | 26.9 | 227 | 4 | US-08-706-945D-14 |
| 16 | 305 | 26.9 | 227 | 4 | US-08-577-788C-48 |
| 17 | 305 | 26.9 | 227 | 4 | US-09-326-394-4 |
| 18 | 305 | 26.9 | 235 | 4 | US-09-580-235-2 |
| 19 | 305 | 26.9 | 235 | 4 | US-09-580-235-8 |
| 20 | 305 | 26.9 | 235 | 4 | US-09-580-181-2 |
| 21 | 305 | 26.9 | 235 | 4 | US-09-580-181-8 |
| 22 | 305 | 26.9 | 235 | 4 | US-09-102-530-2 |
| 23 | 305 | 26.9 | 235 | 4 | US-09-102-530-8 |
| 24 | 305 | 26.9 | 257 | 4 | US-09-579-845-10 |
| 25 | 305 | 26.9 | 461 | 1 | US-08-385-229-2 |
| 26 | 305 | 26.9 | 461 | 1 | US-08-650-000-2 |
| 27 | 305 | 26.9 | 461 | 3 | US-09-042-785A-7 |

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| 28 | 305 | 26.9 | 461 | 3 | US-08-477-347-3 | Sequence 3, Appl1 |
| 29 | 305 | 26.9 | 461 | 3 | US-09-006-353A-4 | Sequence 4, Appl1 |
| 30 | 305 | 26.9 | 461 | 3 | US-08-476-862-2 | Sequence 2, Appl1 |
| 31 | 305 | 26.9 | 461 | 4 | US-09-573-986-4 | Sequence 4, Appl1 |
| 32 | 305 | 26.9 | 461 | 4 | US-08-406-824A-2 | Sequence 2, Appl1 |
| 33 | 305 | 26.9 | 461 | 4 | US-09-800-909-2 | Sequence 2, Appl1 |
| 34 | 305 | 26.9 | 461 | 4 | US-09-758-124-2 | Sequence 2, Appl1 |
| 35 | 305 | 26.9 | 461 | 4 | US-09-800-908-3 | Sequence 2, Appl1 |
| 36 | 305 | 26.9 | 461 | 6 | 5395760-2 | Sequence 3, Appl1 |
| 37 | 305 | 26.9 | 486 | 1 | US-08-243-010-1 | Patent No. 3393760 |
| 38 | 305 | 26.9 | 518 | 1 | US-08-385-229-4 | Sequence 1, Appl1 |
| 39 | 305 | 26.9 | 518 | 4 | US-09-579-845-1 | Sequence 4, Appl1 |
| 40 | 305 | 26.9 | 518 | 4 | US-09-579-845-3 | Sequence 3, Appl1 |
| 41 | 304 | 26.8 | 235 | 4 | US-09-580-235-4 | Sequence 4, Appl1 |
| 42 | 304 | 26.8 | 235 | 4 | US-09-580-235-6 | Sequence 4, Appl1 |
| 43 | 304 | 26.8 | 235 | 4 | US-09-580-181-4 | Sequence 4, Appl1 |
| 44 | 304 | 26.8 | 235 | 4 | US-09-580-181-6 | Sequence 6, Appl1 |
| 45 | 304 | 26.8 | 235 | 4 | US-09-102-530-4 | Sequence 4, Appl1 |

ALIGNMENTS

```
RESULT 1
US-08-505-606-1
; Sequence 1, Application US/08505606
; Patent No. 5925351
;
GENERAL INFORMATION:
; APPLICANT: BROWNING, Jeffrey L.
; APPLICANT: BENJAMIN, Christopher D.
; APPLICANT: HOCHMAN, Paula S.
; TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND
; TITLE OF INVENTION: ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS
; TITLE OF INVENTION: THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr.
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10020
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,606
; FILING DATE: 21-JUL-1995
; CLASSIFICATION: 424
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378,968
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B191
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
;
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-505-606-1
Query Match 100.0%; Score 1133; DB 2; Length 197;
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Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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| Db | 1 | SQPAVAPPYASSENTC | RDOEKEXYEPHOR | ICCSRCPETIYASAKSR | IRDTVCANCAENS | 60 |
| QY | 61 | YNEHMNVYLITCQL | CRPCDPVNGLEBIA | CTSRKTKOGRCPGMFCA | MAALECTHEELLSD | 120 |
| Db | 61 | YNEHMNVYLITCQL | CRPCDPVNGLEBIA | CTSRKTKOGRCPGMFCA | MAALECTHEELLSD | 120 |
| QY | 121 | CPPECTEATLKREY | EKGNNHCVPCKRGH | PONTSSPARGCOPIH | RCENOGIVEAAPTQ | 180 |
| Db | 121 | CPPECTEATLKREY | EKGNNHCVPCKRGH | PONTSSPARGCOPIH | RCENOGIVEAAPTQ | 180 |
| QY | 181 | TTCKNPLEPLPPEMS | SGT | 197 | | |
| Db | 181 | TTCKNPLEPLPPEMS | SGT | 197 | | |

RESULT 2
US-09-000-166-1

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? Sequence 1 Application US/03000166A
? Patent No. 6403087
? GENERAL INFORMATION:
? APPLICANT: BROWNING, et al.
? TITLE OF INVENTION: Soluble Lymphotoxin-B Receptors and Anti-Lymphotoxin
? TITLE OF INVENTION: Receptor and Ligand Antipoddes, as Therapeutic Agents
? TITLE OF INVENTION: for the treatment of Immunological Disease.
? FILE REFERENCE: B191
? CURRENT APPLICATION NUMBER: US/09/000.166A
? CURRENT FILING DATE: 1998-06-08
? EARLIER APPLICATION NUMBER: PCT/US96/12010
? EARLIER FILING DATE: 1996-07-19
? NUMBER OF SEQ ID NOS: 3
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1
? LENGTH: 197
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-000-166-1

Query Match          100.0%;   Score 1133;   DB 4;   length 197;
Best Local Similarity 100.0%;   Pred. No 2.5e-99;
Matches 197;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0,

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RESULT 3
 US-09-303-262-1
 ; Sequence 1, Application US/09303262
 ; Patent No. 6669941
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: BROWNING, Jeffrey L.
 ; BENJAMIN, Christopher D.
 ;
 ; HOCHMAN, Paula S.
 ;
 ; TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND
 ; ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS

THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL DISEASE

NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS: 1
 ADDRESSEE: James F. Haley, Jr.
 CITY: New York
 STREET: 1251 Avenue of the Americas
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Ver
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/303,262
 FILING DATE: 30-Apr-1999
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/505,606
 FILING DATE: 21-Jul-1995
 APPLICATION NUMBER: US 08/378,968
 FILING DATE: 26-Jan-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: HALEY, Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: B191
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 TELEX: 14-8367
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-303-262-1

| | Query Match | 100.0% | Score 1133 | DB 4 | Length 197 | |
|----|-----------------------|---|-------------------|--------------|------------|--------|
| | Best Local Similarity | 100.0% | Pred. No. 2.5e-99 | | | |
| | Matches 197 | Conservative | 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 1 | SQPAVPPYASAEQNTCRDOEKEYYEPQHRICCSRCPEGTYYSAKCSRIIDTVCATCAENS | 60 | | | |
| Db | 1 | SQPAVPPYASAEQNTCRDOEKEYYEPQHRICCSRCPEGTYYSAKCSRIIDTVCATCAENS | 60 | | | |
| QY | 61 | YNEHNNYITITQOLCRPCDPVWNGLEFIACTSRKTKQCCQCGMFCAMALECTHCELLSD | 120 | | | |
| Db | 61 | YNEHNNYITITQOLCRPCDPVWNGLEFIACTSRKTKQCCQCGMFCAMALECTHCELLSD | 120 | | | |
| QY | 121 | CPPTGEALIKDEVGKGNHNCVPCCKAGHFONTISSPSARCOPIHTRCENQGLVEAAPGTAASD | 180 | | | |
| Db | 121 | CPPTGEALIKDEVGKGNHNCVPCCKAGHFONTISSPSARCOPIHTRCENQGLVEAAPGTAASD | 180 | | | |
| QY | 181 | TTCKKNPLELPPEMSGT | 197 | | | |
| Db | 181 | TTCKKNPLELPPEMSGT | 197 | | | |

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RESULT 4
US-08-828-683A-14
; Sequence 14, Application US/08828683A
; Patent No. 6469144
;
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
;
; NUMBER OF SEQUENCES: 28
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

```

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-828-683A-14
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Query Match 87.1%; Score 987; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TCRDQEKYYEPQRIICCSRCPPGTYVSAKSRIRDTVCATCAENSVEHNNYLTICQLC 60

QY 75 RCPDPVWGLIEIAPCTSRKTKQCRCQPMFCAMALBCTHCELLSDCPGTEAEIKDEVG 134
DB 61 RCPDPVWGLIEIAPCTSRKTKQCRCQPMFCAMALBCTHCELLSDCPGTEAEIKDEVG 120

QY 135 KGNHCVCKAGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAOSDTTCK 184
DB 121 KGNHCVCKAGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAOSDTTCK 170

RESULT 5
US-09-523-323-57
Sequence 57, Application US/09523323
Patent No. 6635743

GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan

TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.065000C
CURRENT APPLICATION NUMBER: US/09/523,323
FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/168,380
EARLIER FILING DATE: 1999-12-02
EARLIER APPLICATION NUMBER: 60/148,326
EARLIER FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/142,657
EARLIER FILING DATE: 1999-07-06
EARLIER APPLICATION NUMBER: 60/137,457
EARLIER FILING DATE: 1999-06-04

EARLIER APPLICATION NUMBER: 60/124,041
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: 09/252,656
EARLIER FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: 60/075,409
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/027,287
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/003,886
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 08/822,953
EARLIER FILING DATE: 1997-03-21
EARLIER APPLICATION NUMBER: 60/013,923
EARLIER FILING DATE: 1996-03-22
EARLIER APPLICATION NUMBER: 60/030,157
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: (7)
OTHER INFORMATION: May be any amino acid

US-09-523-323-57

Query Match 86.6%; Score 981; DB 4; Length 170;
Best Local Similarity 99.4%; Pred. No. 4.3e-85;
Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TCRDQEKYYEPQRIICCSRCPPGTYVSAKSRIRDTVCATCAENSVEHNNYLTICQLC 74
DB 1 TCRDQEKYYEPQRIICCSRCPPGTYVSAKSRIRDTVCATCAENSVEHNNYLTICQLC 60

QY 75 RCPDPVWGLIEIAPCTSRKTKQCRCQPMFCAMALBCTHCELLSDCPGTEAEIKDEVG 134
DB 61 RCPDPVWGLIEIAPCTSRKTKQCRCQPMFCAMALBCTHCELLSDCPGTEAEIKDEVG 120

QY 135 KGNHCVCKAGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAOSDTTCK 184
DB 121 KGNHCVCKAGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAOSDTTCK 170

RESULT 6
US-09-006-353A-6
Sequence 6, Application US/09006353A
Patent No. 6261801

GENERAL INFORMATION:
APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN

TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

APPLICANT: Greene, Mark


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? APPLICANT: Murali, Ramachandran
? APPLICANT: Aoki, Kazuhito
? APPLICANT: Baron, Roland
? TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis
? FILE REFERENCE: UPN3832
? CURRENT APPLICATION NUMBER: US/09/627,775
? CURRENT FILING DATE: 2000-07-28
? PRIOR APPLICATION NUMBER: 60/146,090
? PRIOR FILING DATE: 1999-07-28
? NUMBER OF SEQ ID NOS: 29
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 3
? LENGTH: 77
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-627-775-3

Query Match          40.2%; Score 456; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 5.1e-36;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNHNNYLTICQLCRPDPVWGLEIAPCTSKRTQCRQCPGMCAAMALE 111
Db 1 VCATCAENSYNHNNYLTICQLCRPDPVWGLEIAPCTSKRTQCRQCPGMCAAMALE 60
QY 112 CTGCELLSDCPPTGEAR 128
Db 61 CTGCELLSDCPPTGEAR 77

RESULT 10
US-08-974-022-48
? Sequence 48, Application US/08974022
? Patent No. 6015938
? GENERAL INFORMATION:
? APPLICANT: Boyle, William J.
? APPLICANT: Lacey, David L.
? APPLICANT: Calzone, Frank J.
? APPLICANT: Chang, Ming-Shi
? TITLE OF INVENTION: OSTEOPROTEGERIN
? NUMBER OF SEQUENCES: 53
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Amgen Inc.
? STREET: 1840 Dehavilland Drive
? CITY: Thousand Oaks
? STATE: California
? COUNTRY: USA
? ZIP: 91320-1789
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/974,022
? FILING DATE: 12-DEC-1995
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/577,788
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Winter, Robert B.
? REFERENCE/DOCKET NUMBER: A-378
? INFORMATION FOR SEQ ID NO: 48:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 227 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-974-022-48

Query Match          26.9%; Score 305; DB 3; Length 227;
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Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NOTCDQKEKYEYEPQHRICRCPPGTYSVAKCSIRDTVCATCAENSUNE 63
Db 28 AFTPYAPBPGSTCR--LREYYDQTAQMCCKSPQGHAKVFTCTKTSIDTVCSDBSTYQ 85
QY 64 HNNYLTICQLCR---PCDPVWGLEIAPCTSKRTQCRQCPGMCAAMALE-CTHCELLS 119
Db 86 LNNWVECLSCGSSSDQV---ETQACTREQNRICTCRPGWCALSKQSGCRICAPLR 141
QY 120 DCPPG-----TEAEIKDEVGKNNHCVPCKAGHPONTSSPARCQPHTRCENQGLVEAP 174
Db 142 KCRPGFVARPGTETSDV-----CKPCAGTSTNTSSIDICRPHDICN---VVAIP 191
QY 175 GTAQSDITTC--KNLEPLPP 192
Db 192 GNASRDVCTSTSTPSMAP 211

RESULT 11
US-08-795-445A-48
? Sequence 48, Application US/08795445A
? Patent No. 6284485
? GENERAL INFORMATION:
? APPLICANT: Boyle, William J.
? APPLICANT: Lacey, David L.
? APPLICANT: Calzone, Frank J.
? APPLICANT: Chang, Ming-Shi
? TITLE OF INVENTION: OSTEOPROTEGERIN
? NUMBER OF SEQUENCES: 53
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Amgen Inc.
? STREET: 1840 Dehavilland Drive
? CITY: Thousand Oaks
? STATE: California
? COUNTRY: USA
? ZIP: 91320-1789
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/795,445A
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/577,788
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Winter, Robert B.
? REFERENCE/DOCKET NUMBER: A-378
? INFORMATION FOR SEQ ID NO: 48:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 227 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-795-445A-48

Query Match          26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
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QY 120 DCPG-----TEAEIKDEYKGNHCVCKAGHPONTSSPSARCOPIHRCENOGIVEAP 174
Db 142 KCRPGGVARPGTETSVDV-----CKPCAPGTFSNTTSSDTCRPHQICN-----VVAIP 191
QY 175 GTAOSDTTC--KNPLEPLRP 192
Db 192 GNASRDVACTSTSPTRSMAP 211

RESULT 12
US-08-795-447A-48
; Sequence 48, Application US/08795447A
; Patent No. 6284728

GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91362-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378D2
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-447A-48

Query Match 26.9%; Score 305; DB 3; Length 227;

Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NOTCRDOKEEYEPQRIICSRCPGTYVSACSRIRDTVCATCAENSYNE 63
Db 28 AFTPYAEPBPGSTCR--LREYYDQTAQWCCSKCSPGQIAKVFCTKTSIDVDCSCDSTYTQ 85
QY 64 HNNYLTICQLCR---PCDPVNGLEIEIACTSKRKTQCRQCPGMFCAMALE-CTHCELLS 119
Db 86 LMNWVPECLSCGSRSSDQV---ETQACTREONRICTCRPGWYCALSKQEGCRICAPLR 141
QY 120 DCPG-----TEAEIKDEYKGNHCVCKAGHPONTSSPSARCOPIHRCENOGIVEAP 174
Db 142 KCRPGGVARPGTETSVDV-----CKPCAPGTFSNTTSSDTCRPHQICN-----VVAIP 191
QY 175 GTAOSDTTC--KNPLEPLRP 192
Db 192 GNASRDVACTSTSPTRSMAP 211

RESULT 13
US-08-974-186-48
; Sequence 48, Application US/08974186

Patent No. 6284740
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-186-48

Query Match 26.9%; Score 305; DB 3; Length 227;

Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NOTCRDOKEEYEPQRIICSRCPGTYVSACSRIRDTVCATCAENSYNE 63
Db 28 AFTPYAEPBPGSTCR--LREYYDQTAQWCCSKCSPGQIAKVFCTKTSIDVDCSCDSTYTQ 85
QY 64 HNNYLTICQLCR---PCDPVNGLEIEIACTSKRKTQCRQCPGMFCAMALE-CTHCELLS 119
Db 86 LMNWVPECLSCGSRSSDQV---ETQACTREONRICTCRPGWYCALSKQEGCRICAPLR 141
QY 120 DCPG-----TEAEIKDEYKGNHCVCKAGHPONTSSPSARCOPIHRCENOGIVEAP 174
Db 142 KCRPGGVARPGTETSVDV-----CKPCAPGTFSNTTSSDTCRPHQICN-----VVAIP 191
QY 175 GTAOSDTTC--KNPLEPLRP 192
Db 192 GNASRDVACTSTSPTRSMAP 211

RESULT 14
US-08-795-446B-48

; Sequence 48, Application US/08795446B
; Patent No. 6288032

GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.

STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-446B-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTCRDOEKEYEPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENS YNE 63
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Db 28 APTPYADEPGSTCR-LREYIDQTAQWCCSKSPGQAHKVFCTKTSIDVCDSCEDSTYTQ 85
QY 64 HNNYLTICQLCR---PCDPYMGLEBIACTSKRKTQCRQPGMFCAMALE-CTHCELLS 119
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Db 86 LMNWPVECLSGSRCSQV---ETQACTREQNRICTRPGWYCALSKQEGCLCAPLR 141
QY 120 DCPPG-----TEAEIKDEVGKGNHCVPCAKGHFQNTSSPSARCOPTHRCENQGLVEAP 174
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Db 142 KCRPGFGVAPRGTEISDVV-----CKPCAPGTFSTNTSTDICRPHQICN---VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLP 192
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Db 192 GNASRDVCTSTSPTRSMAP 211

RESULT 15
US-08-706-945D-134
Sequence 134, Application US/08706945D
Patent No. 6369027
GENERAL INFORMATION:
APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
PRIOR FILING DATE: 1996-09-03
CURRENT APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patent in version 3.1
SEQ ID NO 134
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-08-706-945D-134

Query Match 26.9%; Score 305; DB 4; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
QY 5 AVPPYASE-NQTCRDOEKEYEPQHRICCSRCPGTYVSAKCSRIRDTVCATCAENS YNE 63
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Db 28 APTPYADEPGSTCR-LREYIDQTAQWCCSKSPGQAHKVFCTKTSIDVCDSCEDSTYTQ 85
QY 64 HNNYLTICQLCR---PCDPYMGLEBIACTSKRKTQCRQPGMFCAMALE-CTHCELLS 119
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| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 86 LMNWPVECLSGSRCSQV---ETQACTREQNRICTRPGWYCALSKQEGCLCAPLR 141
QY 120 DCPPG-----TEAEIKDEVGKGNHCVPCAKGHFQNTSSPSARCOPTHRCENQGLVEAP 174
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| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 142 KCRPGFGVAPRGTEISDVV-----CKPCAPGTFSTNTSTDICRPHQICN---VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLP 192
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Db 192 GNASRDVCTSTSPTRSMAP 211

Search completed: August 28, 2004, 01:50:54
Job time : 33 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 01:47:13 ; Search time 125 Seconds
(without alignments)
495.830 Million cell updates/sec

Title: US-10-003-211-1
Perfect score: 1133
Sequence: 1 SOPQAVPPYASENQCRDQE.....QSDPTCKNPLEPPEMSGR 197

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Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
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| 2 | 1133 | 100.0 | 435 | 9 | US-09-907-372-19 |
| 3 | 1133 | 100.0 | 435 | 9 | US-09-768-779A-6 |
| 4 | 1133 | 100.0 | 435 | 10 | US-09-917-372-19 |
| 5 | 1133 | 100.0 | 435 | 12 | US-10-087-192-942 |
| 6 | 1133 | 100.0 | 435 | 14 | US-10-291-480-6 |
| 7 | 1133 | 100.0 | 435 | 15 | US-10-369-300-17 |
| 8 | 1133 | 100.0 | 435 | 15 | US-10-262-445-133 |
| 9 | 1129 | 99.6 | 339 | 9 | US-09-907-372-1 |
| 10 | 1129 | 99.6 | 339 | 10 | US-09-917-372-1 |
| 11 | 987 | 87.1 | 170 | 13 | US-10-112-793-14 |
| 12 | 970 | 85.6 | 172 | 15 | US-10-375-680-57 |
| 13 | 780 | 68.8 | 257 | 9 | US-09-948-018-19 |
| 14 | 771 | 68.0 | 402 | 12 | US-10-087-192-939 |
| 15 | 771 | 68.0 | 415 | 9 | US-09-826-212-6 |

| | | | | | | |
|----|-------|------|-----|----|--------------------|-------------------|
| 16 | 771 | 68.0 | 415 | 9 | US-09-907-372-20 | Sequence 20, Appl |
| 17 | 771 | 68.0 | 415 | 9 | US-09-935-727-8 | Sequence 8, Appl |
| 18 | 771 | 68.0 | 415 | 10 | US-09-917-372-20 | Sequence 20, Appl |
| 19 | 771 | 68.0 | 415 | 14 | US-10-186-643-6 | Sequence 6, Appl |
| 20 | 771 | 68.0 | 415 | 15 | US-10-418-242-8 | Sequence 8, Appl |
| 21 | 381.5 | 33.7 | 305 | 15 | US-10-264-049-3058 | Sequence 3058, Ap |
| 22 | 311.5 | 27.5 | 659 | 14 | US-10-363-427-12 | Sequence 12, Appl |
| 23 | 307 | 27.1 | 720 | 14 | US-10-363-427-8 | Sequence 8, Appl |
| 24 | 305 | 26.9 | 225 | 9 | US-09-840-795-10 | Sequence 10, Appl |
| 25 | 305 | 26.9 | 227 | 11 | US-09-405-032-131 | Sequence 131, App |
| 26 | 305 | 26.9 | 235 | 9 | US-09-907-263-4 | Sequence 4, Appl |
| 27 | 305 | 26.9 | 235 | 10 | US-09-882-735-16 | Sequence 16, Appl |
| 28 | 305 | 26.9 | 235 | 12 | US-10-621-783-4 | Sequence 4, Appl |
| 29 | 305 | 26.9 | 235 | 12 | US-10-622-383-4 | Sequence 4, Appl |
| 30 | 305 | 26.9 | 235 | 14 | US-10-243-230-8 | Sequence 8, Appl |
| 31 | 305 | 26.9 | 235 | 14 | US-10-313-826-75 | Sequence 75, Appl |
| 32 | 305 | 26.9 | 257 | 14 | US-10-313-852-10 | Sequence 10, Appl |
| 33 | 305 | 26.9 | 257 | 14 | US-10-314-033-10 | Sequence 10, Appl |
| 34 | 305 | 26.9 | 439 | 15 | US-10-360-101-226 | Sequence 226, App |
| 35 | 305 | 26.9 | 450 | 9 | US-09-768-779A-3 | Sequence 3, Appl |
| 36 | 305 | 26.9 | 450 | 14 | US-10-291-480-3 | Sequence 3, Appl |
| 37 | 305 | 26.9 | 461 | 9 | US-09-800-909-2 | Sequence 2, Appl |
| 38 | 305 | 26.9 | 461 | 9 | US-09-826-212-4 | Sequence 4, Appl |
| 39 | 305 | 26.9 | 461 | 9 | US-09-758-124-2 | Sequence 2, Appl |
| 40 | 305 | 26.9 | 461 | 9 | US-09-896-096A-17 | Sequence 17, Appl |
| 41 | 305 | 26.9 | 461 | 9 | US-09-894-924-17 | Sequence 17, Appl |
| 42 | 305 | 26.9 | 461 | 9 | US-09-840-707A-17 | Sequence 17, Appl |
| 43 | 305 | 26.9 | 461 | 9 | US-09-800-908-3 | Sequence 3, Appl |
| 44 | 305 | 26.9 | 461 | 9 | US-09-935-727-6 | Sequence 6, Appl |
| 45 | 305 | 26.9 | 461 | 9 | US-09-935-727-6 | Sequence 6, Appl |

ALIGNMENTS

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RESULT 1
US-10-003-211-1
; Publication 1, Application US/10003211
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Soluble Lymphotoxin Beta Receptor and
; Anti-Lymphotoxin Receptor and Ligand Antibodies as
; TITLE OF INVENTION: Therapeutic Agents for the Treatment of Immunological
; FILE REFERENCE: A013US
; CURRENT APPLICATION NUMBER: US/10/003,211
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: PCT/US97/19436
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/029,060
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-003-211-1
Query Match 100.0%; Score 1133; DB 13; Length 197;
Best Local Similarity 100.0%; Pred. No. 7.6e-89;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOPQAVPPYASENQCRDQKEYEPDHRICRCRCPGTVYSAKCSRIKDTVCATCAENS 60
Db 1 SOPQAVPPYASENQCRDQKEYEPDHRICRCRCPGTVYSAKCSRIKDTVCATCAENS 60
QY 61 YNHNMYLITTCQCRPCDPMGLEETAPCTSRKTKTCRCPGMFCAMALECHTCLSTD 120
Db 61 YNHNMYLITTCQCRPCDPMGLEETAPCTSRKTKTCRCPGMFCAMALECHTCLSTD 120
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QY 121 CPPTGTEALKDVEVGKNNHCVPCKAGHFONTSSPSARCQPHTRCENOGIVEAAGTAQSD 180
 DB 121 CPPTGTEALKDVEVGKNNHCVPCKAGHFONTSSPSARCQPHTRCENOGIVEAAGTAQSD 180
 QY 181 TTCKNPLEPLPPEMSGT 197
 DB 181 TTCKNPLEPLPPEMSGT 197

RESULT 2
 US-09-907-372-19
 ; Sequence 19, Application US/09907372
 ; Patent No. US20020068242A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal, Preeti G.
 ; APPLICANT: Warren, Bridget A.
 ; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
 ; FILE REFERENCE: PC-0050 US
 ; CURRENT APPLICATION NUMBER: US/09/907,372
 ; CURRENT FILING DATE: 2001-07-27
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 19
 ; LENGTH: 435
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020068242A1 g339762
 ; US-09-907-372-19

Query Match 100.0%; Score 1133; DB 9; Length 435;
 Best Local Similarity 100.0%; Pred. No. 1.7e-88;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIIDTVCAATCAENS 60
 DB 28 SOPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIIDTVCAATCAENS 87
 QY 61 YNEHMYNTLTICQLCRPCDPVWGLEIAPCTSKRTKTCRCQPGMCAAMALECTHCELLSD 120
 DB 88 YNEHMYNTLTICQLCRPCDPVWGLEIAPCTSKRTKTCRCQPGMCAAMALECTHCELLSD 147
 QY 121 CPPTGTEALKDVEVGKNNHCVPCKAGHFONTSSPSARCQPHTRCENOGIVEAAGTAQSD 180
 DB 148 CPPTGTEALKDVEVGKNNHCVPCKAGHFONTSSPSARCQPHTRCENOGIVEAAGTAQSD 207
 QY 181 TTCKNPLEPLPPEMSGT 197
 DB 208 TTCKNPLEPLPPEMSGT 224

RESULT 3
 US-09-768-779A-6
 ; Sequence 6, Application US/09768779A
 ; Patent No. US20020127637A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, JIAN
 ; APPLICANT: MOORE, PAUL
 ; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
 ; RECEPTOR-LIKE PROTEIN 8
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: HUMAN GENOME SCIENCES, INC.
 ; STREET: 9410 KEY WEST AVENUE
 ; CITY: ROCKVILLE
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/768,779A
 ; FILING DATE: 25-Jan-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/086,582
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KENTLEY K. HOOVER
 ; REGISTRATION NUMBER: 40,302
 ; REFERENCE/DOCKET NUMBER: PF368PP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8439
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 435 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 ; US-09-768-779A-6

Query Match 100.0%; Score 1133; DB 9; Length 435;
 Best Local Similarity 100.0%; Pred. No. 1.7e-88;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIIDTVCAATCAENS 60
 DB 28 SOPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIIDTVCAATCAENS 87
 QY 61 YNEHMYNTLTICQLCRPCDPVWGLEIAPCTSKRTKTCRCQPGMCAAMALECTHCELLSD 120
 DB 88 YNEHMYNTLTICQLCRPCDPVWGLEIAPCTSKRTKTCRCQPGMCAAMALECTHCELLSD 147
 QY 121 CPPTGTEALKDVEVGKNNHCVPCKAGHFONTSSPSARCQPHTRCENOGIVEAAGTAQSD 180
 DB 148 CPPTGTEALKDVEVGKNNHCVPCKAGHFONTSSPSARCQPHTRCENOGIVEAAGTAQSD 207
 QY 181 TTCKNPLEPLPPEMSGT 197
 DB 208 TTCKNPLEPLPPEMSGT 224

RESULT 4
 US-09-917-372-19
 ; Sequence 19, Application US/09917372
 ; Publication No. US20030068619A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal, Preeti G.
 ; APPLICANT: Warren, Bridget A.
 ; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
 ; FILE REFERENCE: PC-0050 US
 ; CURRENT APPLICATION NUMBER: US/09/917,372
 ; CURRENT FILING DATE: 2002-09-09
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 19
 ; LENGTH: 435
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030068619A1 g339762
 ; US-09-917-372-19

Query Match 100.0%; Score 1133; DB 10; Length 435;
 Best Local Similarity 100.0%; Pred. No. 1.7e-88;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIIDTVCAATCAENS 60

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Db      ||| 28 SGPQAVPPYASENQTCRDOEKEYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 87
Qy      ||| 61 YNEHWNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQGMFCAMALECTHCELLSD 120
Db      ||| 88 YNEHWNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQGMFCAMALECTHCELLSD 147
Qy      ||| 121 CPGTEAELKDEVGKGNHCVPCAKAGHFONTSSPSARQPHTRCENGLVEAAGTAQSD 180
Db      ||| 148 CPGTEAELKDEVGKGNHCVPCAKAGHFONTSSPSARQPHTRCENGLVEAAGTAQSD 207
Qy      ||| 181 TTCNPLEPLPPEMSGT 197
Db      ||| 208 TTCNPLEPLPPEMSGT 224
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RESULT 5

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US-10-087-192-942
; Sequence 942, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 942
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-942
```

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Query Match      100.0%; Score 1133; DB 12; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGPQAVPPYASENQTCRDOEKEYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 60
Db      28 SGPQAVPPYASENQTCRDOEKEYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 87
Qy      61 YNEHWNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQGMFCAMALECTHCELLSD 120
Db      88 YNEHWNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQGMFCAMALECTHCELLSD 147
Qy      121 CPGTEAELKDEVGKGNHCVPCAKAGHFONTSSPSARQPHTRCENGLVEAAGTAQSD 180
Db      148 CPGTEAELKDEVGKGNHCVPCAKAGHFONTSSPSARQPHTRCENGLVEAAGTAQSD 207
Qy      181 TTCNPLEPLPPEMSGT 197
Db      208 TTCNPLEPLPPEMSGT 224
```

```
RESULT 6
US-10-291-480-6
; Sequence 6, Application US/10291480
; Publication No. US20030100069A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8
; FILE REFERENCE: P368C1D1
; CURRENT APPLICATION NUMBER: US/10/291,480
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/768,779
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; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/086,582
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/048,020
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 435
; TYPE: PRT
; ORGANISM: human
US-10-291-480-6
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Query Match      100.0%; Score 1133; DB 14; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SGPQAVPPYASENQTCRDOEKEYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 60
Db      28 SGPQAVPPYASENQTCRDOEKEYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 87
Qy      61 YNEHWNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQGMFCAMALECTHCELLSD 120
Db      88 YNEHWNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQGMFCAMALECTHCELLSD 147
Qy      121 CPGTEAELKDEVGKGNHCVPCAKAGHFONTSSPSARQPHTRCENGLVEAAGTAQSD 180
Db      148 CPGTEAELKDEVGKGNHCVPCAKAGHFONTSSPSARQPHTRCENGLVEAAGTAQSD 207
Qy      181 TTCNPLEPLPPEMSGT 197
Db      208 TTCNPLEPLPPEMSGT 224
```

RESULT 7

```
US-10-369-300-17
; Sequence 17, Application US/10369300
; Publication No. US20030215442A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Wayne
; APPLICANT: Frazer, Christopher
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
; TITLE OF INVENTION: IMMUNE
; FILE REFERENCE: 7853-255
; CURRENT APPLICATION NUMBER: US/10/369,300
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/358,463
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-300-17
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```
Query Match      100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 SGPQAVPPYASENQTCRDOEKEYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 60
Db      28 SGPQAVPPYASENQTCRDOEKEYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENS 87
Qy      61 YNEHWNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQGMFCAMALECTHCELLSD 120
Db      88 YNEHWNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQGMFCAMALECTHCELLSD 147
Qy      121 CPGTEAELKDEVGKGNHCVPCAKAGHFONTSSPSARQPHTRCENGLVEAAGTAQSD 180
Db      148 CPGTEAELKDEVGKGNHCVPCAKAGHFONTSSPSARQPHTRCENGLVEAAGTAQSD 207
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QY 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

RESULT 8

US-10-262-445-133
; Sequence 133, Application US/10262445
; Publication No. US20040014058A1
; GENERAL INFORMATION:
; APPLICANT: Alebrock II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Catterton, Elina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Girot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
; FILE REFERENCE: 21402-462D
; CURRENT APPLICATION NUMBER: US/10/262,445
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 133
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-445-133

Query Match 100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIRDIVCATCAENS 60
Db 28 SQPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIRDIVCATCAENS 87

QY 61 YNEHNNYLTICQLCRPCDPVWGLBEIAPCTSKRKTCRCQPGMFCAMALECTHCELLSD 120
Db 88 YNEHNNYLTICQLCRPCDPVWGLBEIAPCTSKRKTCRCQPGMFCAMALECTHCELLSD 147
QY 121 CPGTEALKDVEYKGNHNCVPCAKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTAOSD 180
Db 148 CPGTEALKDVEYKGNHNCVPCAKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTAOSD 207
QY 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

RESULT 9

US-09-907-372-1
; Sequence 1, Application US/09907372
; Patent No. US20020068242A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/907,372
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020068242A1 7497867CD1
US-09-907-372-1

Query Match 99.6%; Score 1129; DB 9; Length 399;
Best Local Similarity 99.5%; Pred. No. 3.5e-88;
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIRDIVCATCAENS 60
Db 28 SQPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIRDIVCATCAENS 87
QY 61 YNEHNNYLTICQLCRPCDPVWGLBEIAPCTSKRKTCRCQPGMFCAMALECTHCELLSD 120
Db 88 YNEHNNYLTICQLCRPCDPVWGLBEIAPCTSKRKTCRCQPGMFCAMALECTHCELLSD 147
QY 121 CPGTEALKDVEYKGNHNCVPCAKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTAOSD 180
Db 148 CPGTEALKDVEYKGNHNCVPCAKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTAOSD 207
QY 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

RESULT 10

US-09-917-372-1
; Sequence 1, Application US/09917372
; Publication No. US20030068619A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/917,372
; CURRENT FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030068619A1 7497867CD1
US-09-917-372-1

Query Match 99.6%; Score 1129; DB 10; Length 399;
Best Local Similarity 99.5%; Pred. No. 3.5e-88;
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGPAAVPPVASENQTCDQKEKEYEPQHRICSRCPPTGVSAKCSRIPTVCATCAENS 60
DB 28 SQDQAVPPVASENQTCDQKEKEYEPQHRICSRCPPTGVSAKCSRIPTVCATCAENS 87
QY 61 YNHNWVLTITCOLCRPCDPVWGJBEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 120
DB 88 YNHNWVLTITCOLCRPCDPVWGJBEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 147
QY 121 CPGTEALKDVEGKGNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAGTAQSD 180
DB 148 CPGTEALKDVEGKGNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAGTAQSD 207
QY 181 TTCKNPLEPLPEMSGT 197
DB 208 TTCKNPLEPLPEMSGS 224

RESULT 11

US-10-112-793-14
Sequence 14, Application US/10112793
Publication No. US20020192729A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 Lf AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-112-793-14

Query Match 87.1%; Score 987; DB 13; Length 170;

Best Local Similarity 100.0%; Pred. No. 1.9e-76;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TCRDQKEYEYEPQHRICSRCPPTGVSAKCSRIPTVCATCAENSYNHNWVLTITCOLC 74
DB 1 TCRDQKEYEYEPQHRICSRCPPTGVSAKCSRIPTVCATCAENSYNHNWVLTITCOLC 60
QY 75 RCPDPMGJBEIAPCTSKRTQCRQPGMFCAMALECTHCELLSDCPGTEALKDVEG 134
DB 61 RCPDPMGJBEIAPCTSKRTQCRQPGMFCAMALECTHCELLSDCPGTEALKDVEG 120
QY 135 KGNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAGTAQSDTTCK 184
DB 121 KGNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAGTAQSDTTCK 170

RESULT 12

US-10-375-680-57
Sequence 57, Application US/10375680
Publication No. US20040009147A1

GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-liang
APPLICANT: Ruden, Steven M
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488, 065000E
CURRENT APPLICATION NUMBER: US/10/375,680
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,234
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.2
SEQ ID NO 57
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (7)-(7)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-375-680-57

Query Match 85.6%; Score 970; DB 15; Length 172;
Best Local Similarity 98.3%; Pred. No. 5.3e-75;
Matches 169; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 15 TCRDQE--KEYEYEPQHRICSRCPPTGVSAKCSRIPTVCATCAENSYNHNWVLTITCQ 72
DB 1 TCRDQEXAAEYEPQHRICSRCPPTGVSAKCSRIPTVCATCAENSYNHNWVLTITCQ 60
QY 73 LCPDPMGJBEIAPCTSKRTQCRQPGMFCAMALECTHCELLSDCPGTEALKDVE 132
DB 61 LCPDPMGJBEIAPCTSKRTQCRQPGMFCAMALECTHCELLSDCPGTEALKDVE 120
QY 133 VGKGNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAGTAQSDTTCK 184
DB 121 VGKGNHCVPCKAGHFONTSSPSARCPHTRCENOGIVEAAGTAQSDTTCK 172

RESULT 13

US-09-948-018-19
Sequence 19, Application US/09948018
Patent No. US20020150977A1

GENERAL INFORMATION:

APPLICANT: Theill et al
TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
FILE REFERENCE: 01017/37677
CURRENT APPLICATION NUMBER: US/09/948,018
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/230,191
PRIOR FILING DATE: 2000-09-05

